

Fig. 1.0

433270 01092860

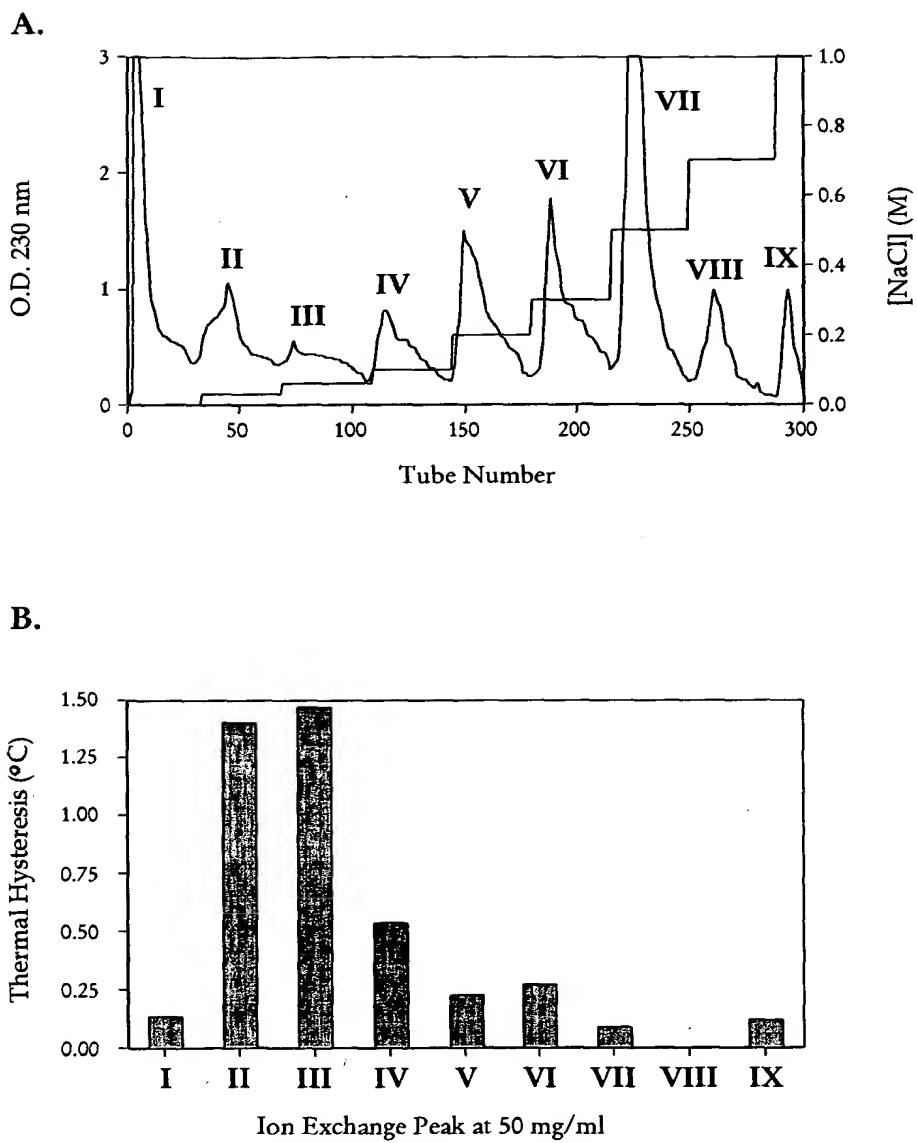


Fig. 1.1

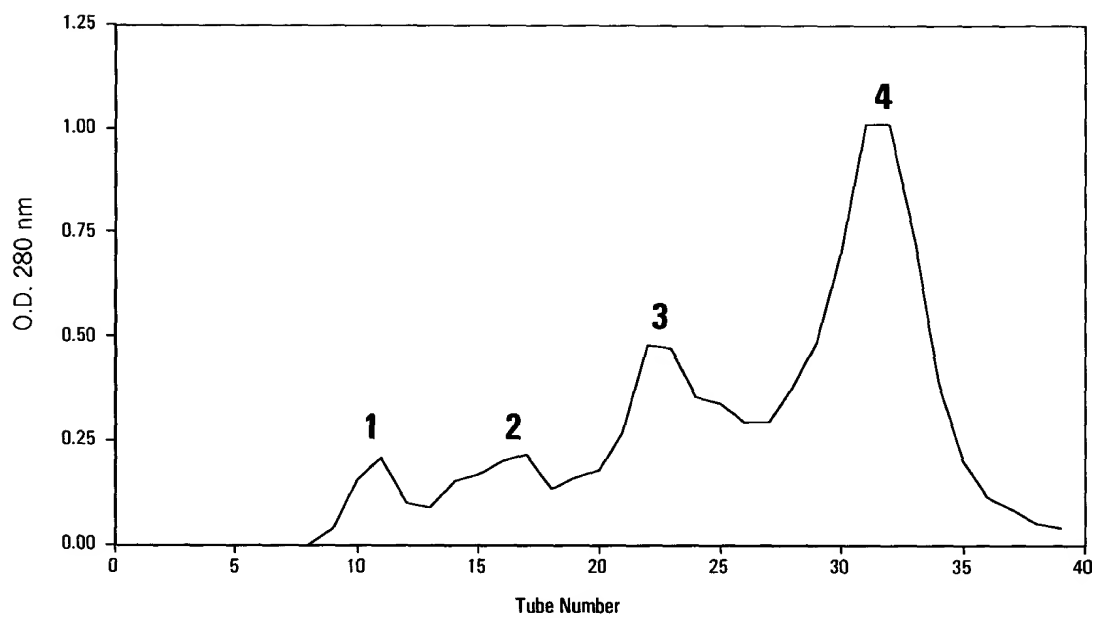


Fig. 1.2

09076349 012393

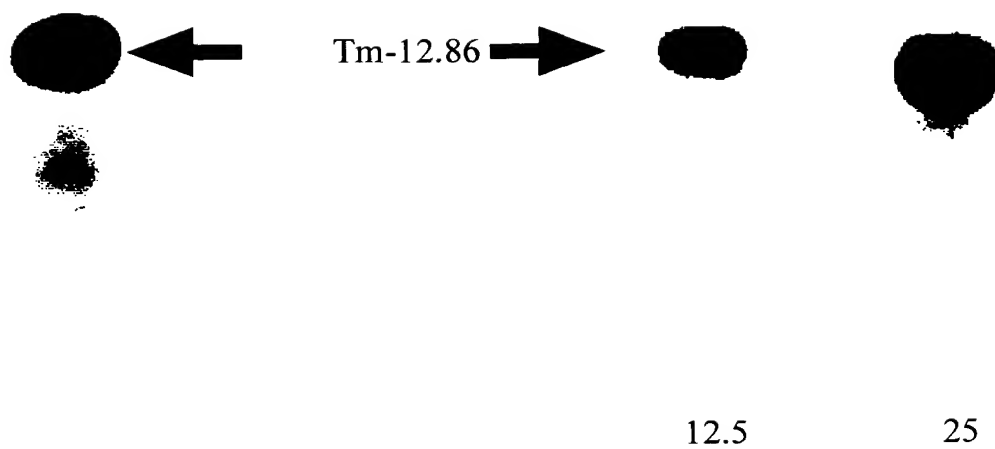


Fig. 1.3

Fig. 1.4

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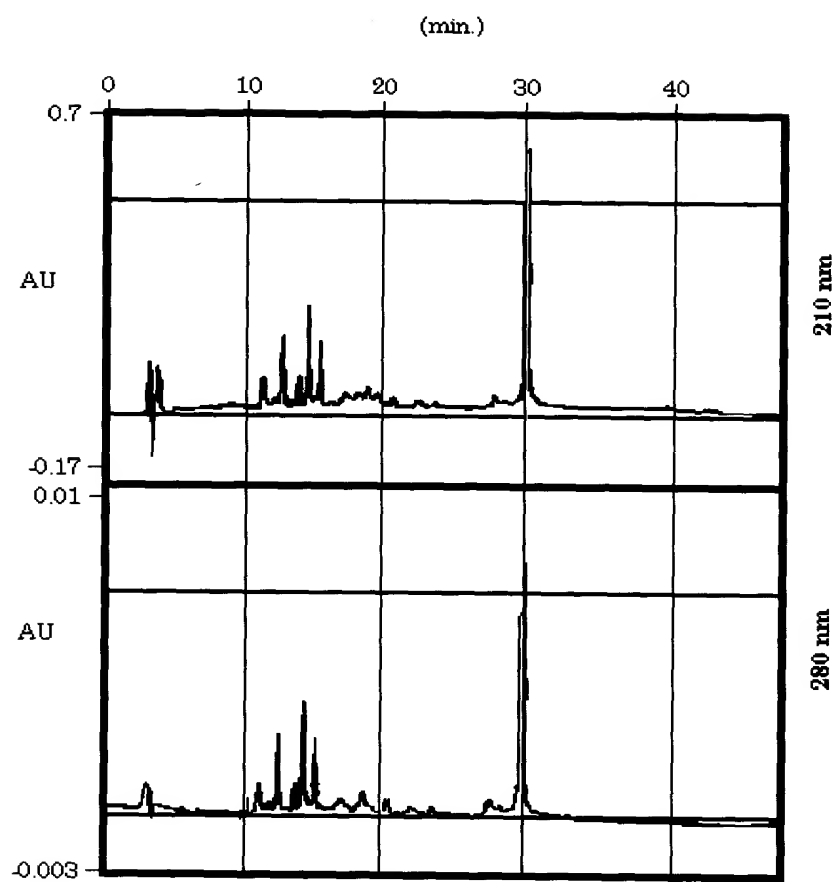


Fig. 1.5

2025-01-23 09:23:23

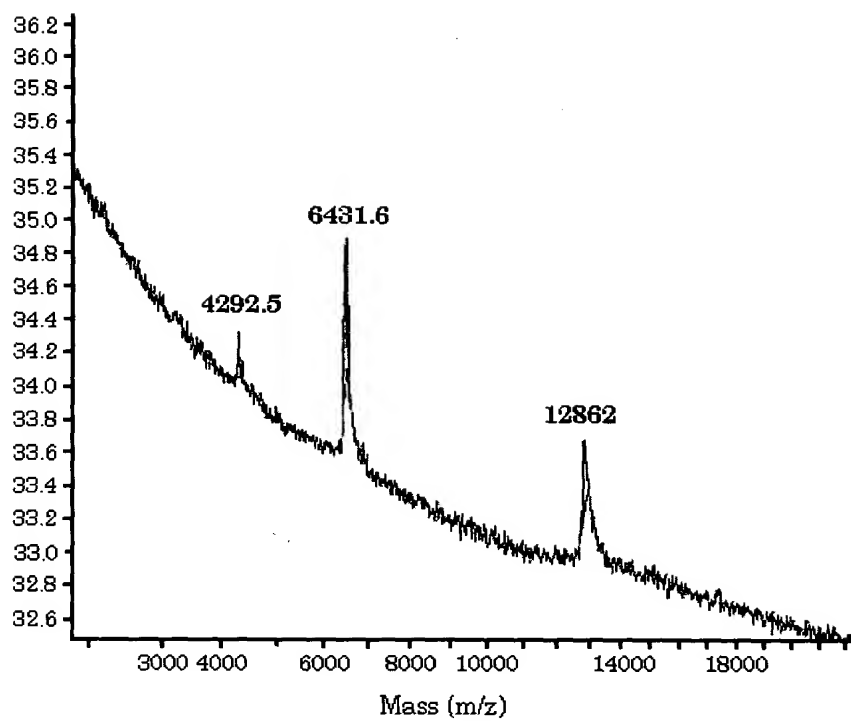


Fig. 1.6

SDS-PAGE gel image showing protein bands for 'w' and 'w/o' conditions. Molecular weight markers are on the left: 16.9, 14.4, 10.7, 8.2, 6.2, and 2.5 kDa. An arrow points to a band in the 'w/o' lane at approximately 12.86 kDa, labeled 'Tm-12.86'.

Fig. 1.7

09075340 015000

NH₂-L-T-D-E-Q-I-Q-K-R-N-K-I-S-K-E-?-Q-Q-V

Val
Gln
Gln
Gln
Lys
Ser
Ile
Lys
Asn
Arg
Lys
Gln
Ile
Gln
Glu
Asp
Thr
Leu

Fig. 1.8

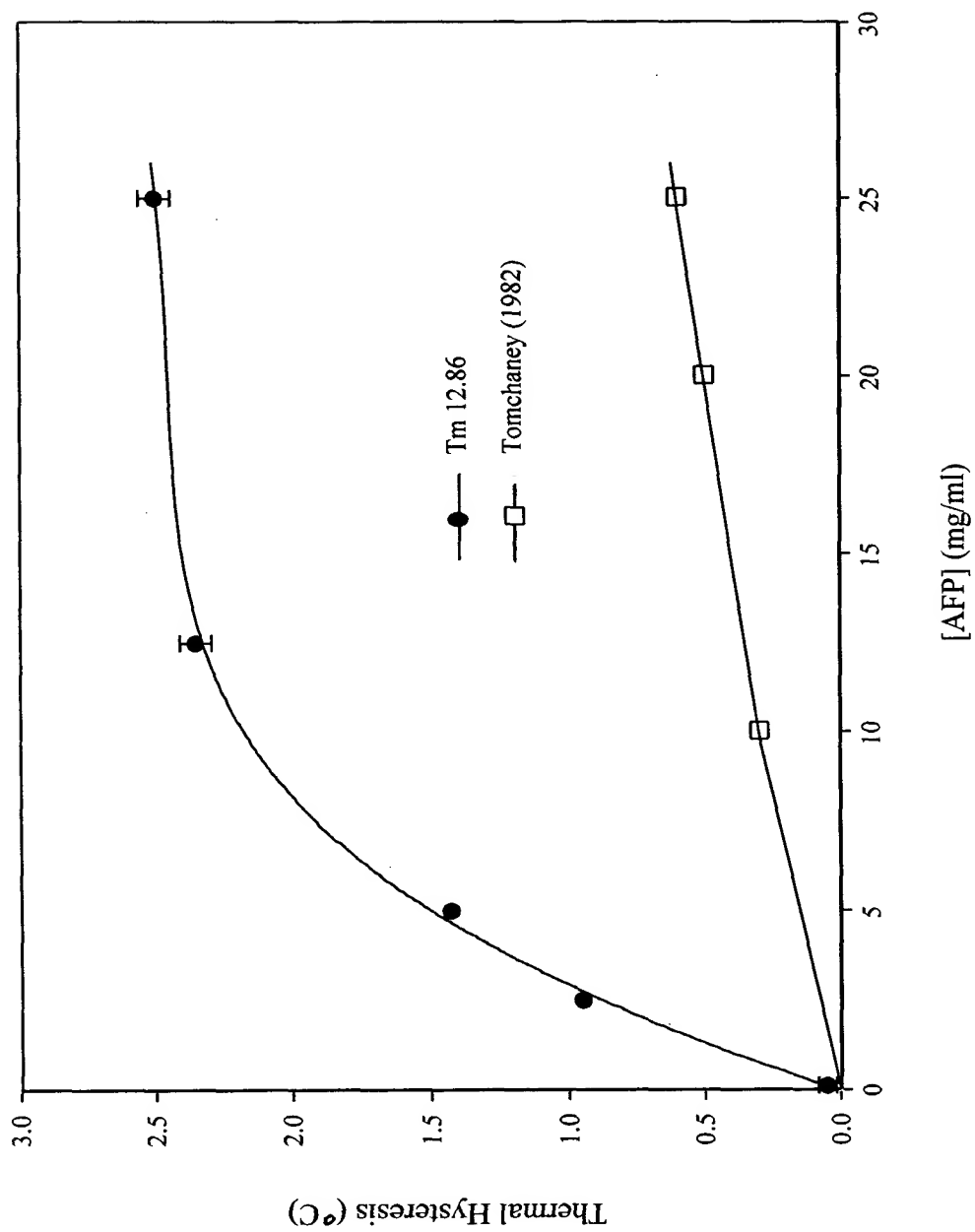


Fig. 1.9

203270-0152360

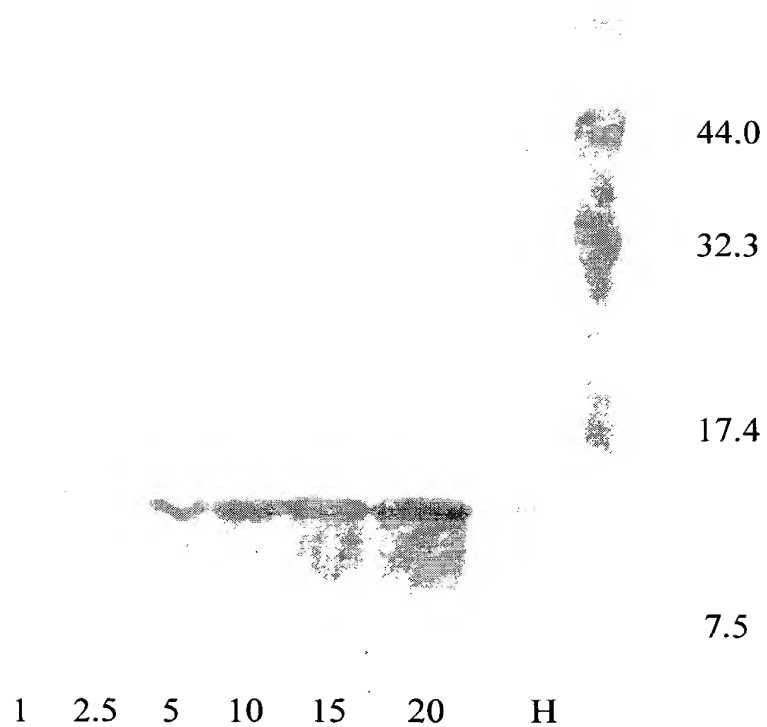


Fig. 1.10

20250408 09:22:30

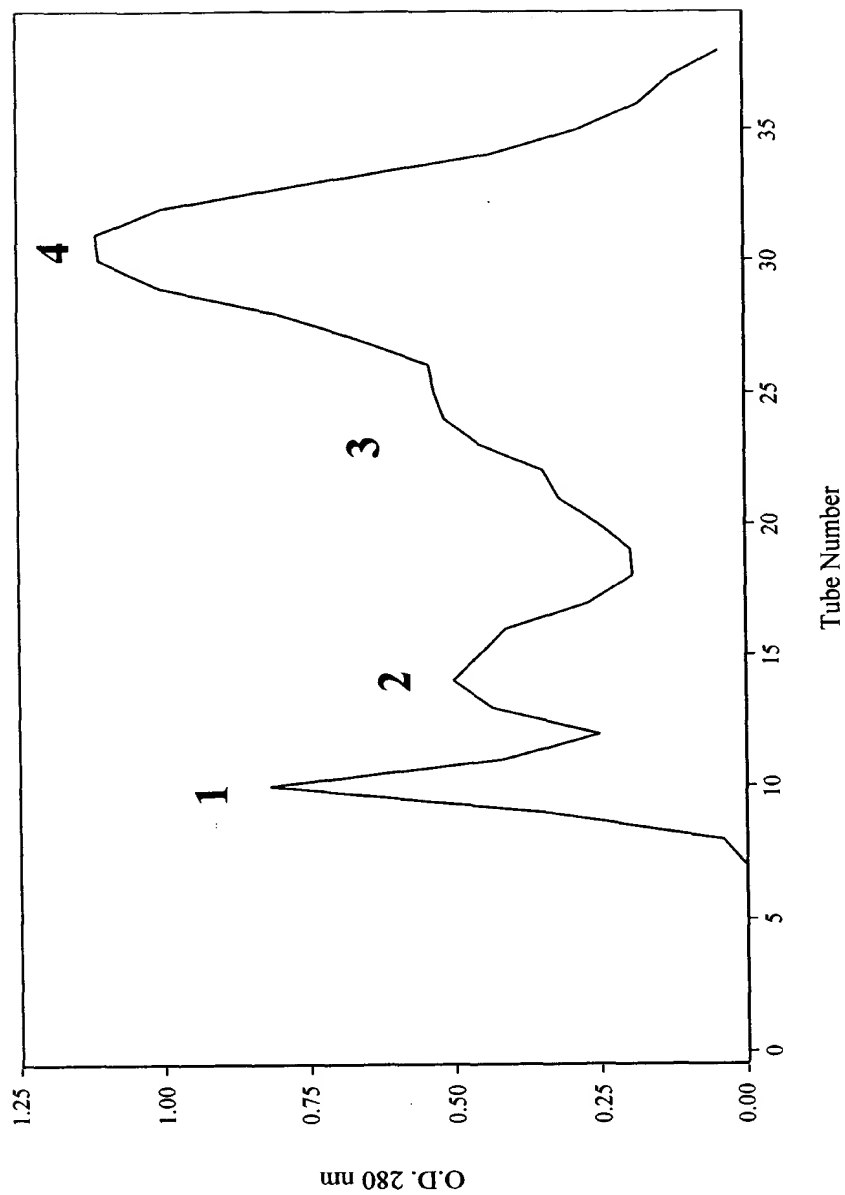


Fig. 1.11

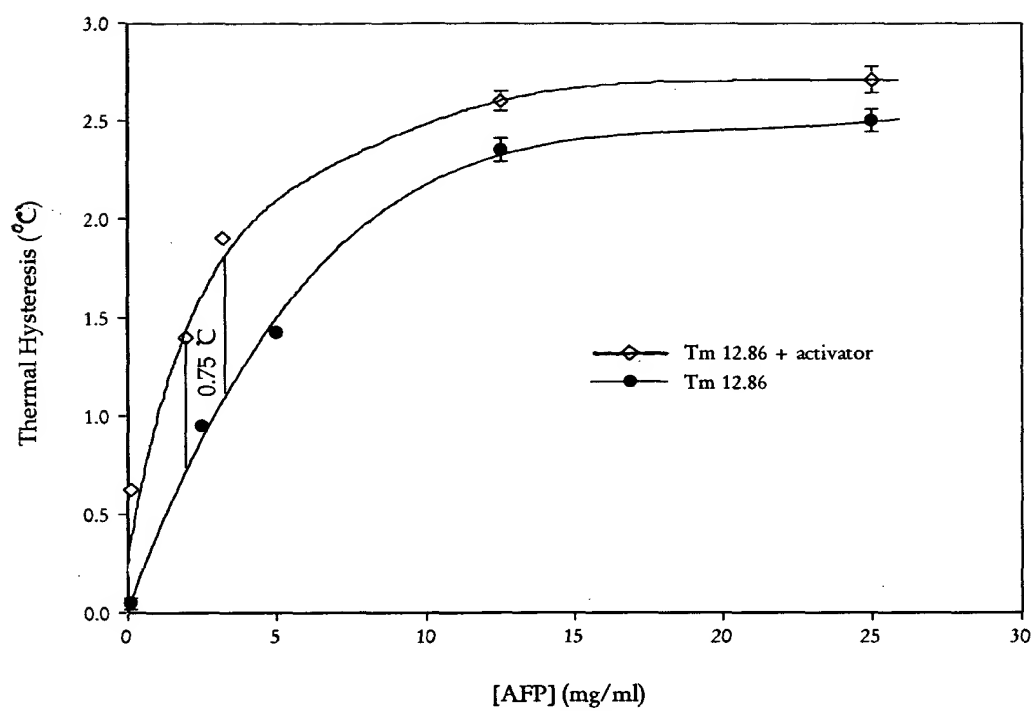


Fig. 1.12

200210" 01E92860

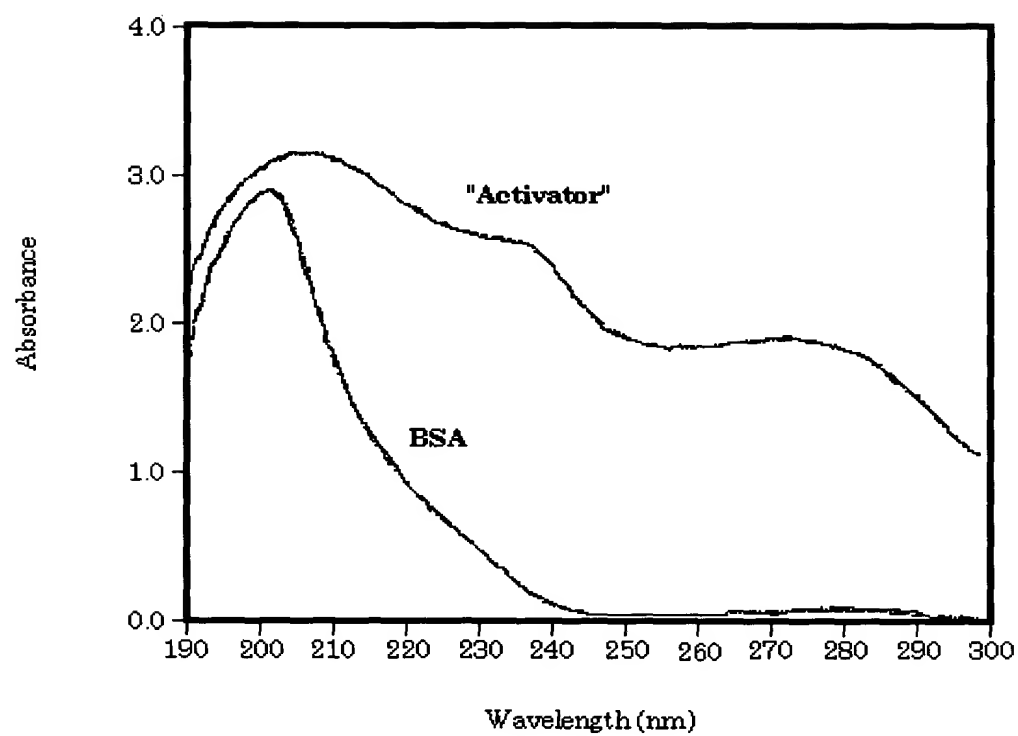


Fig. 1.13

0907348.01203

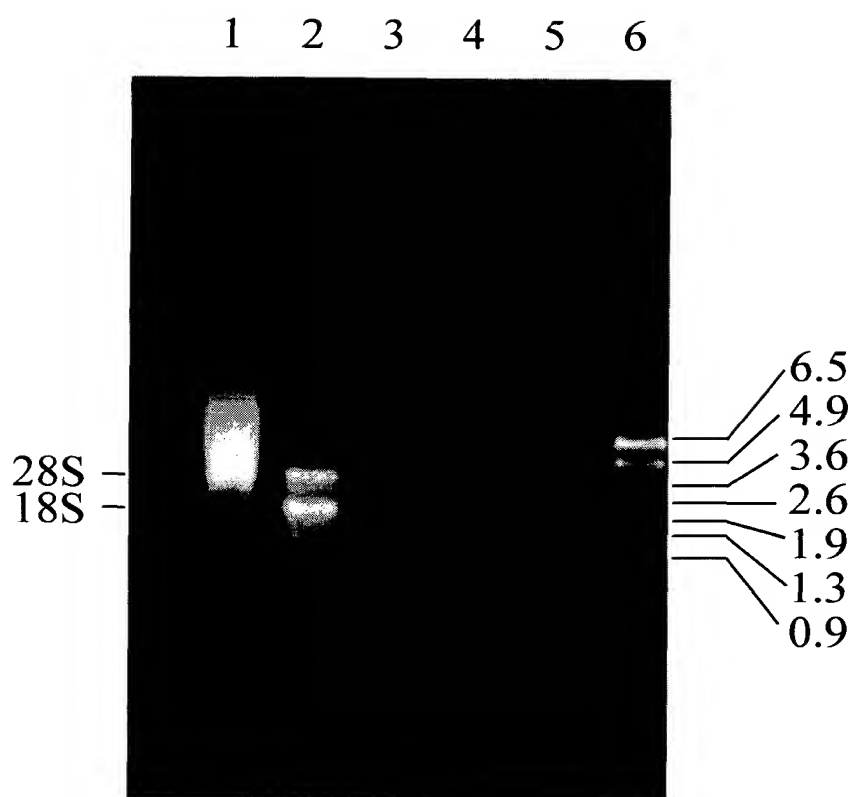


Fig. 2.0

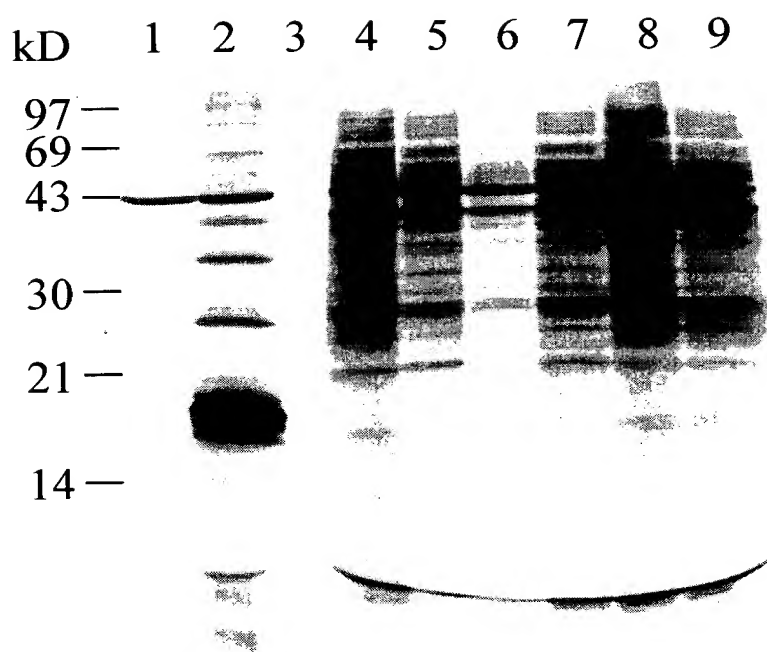


Fig. 2.1

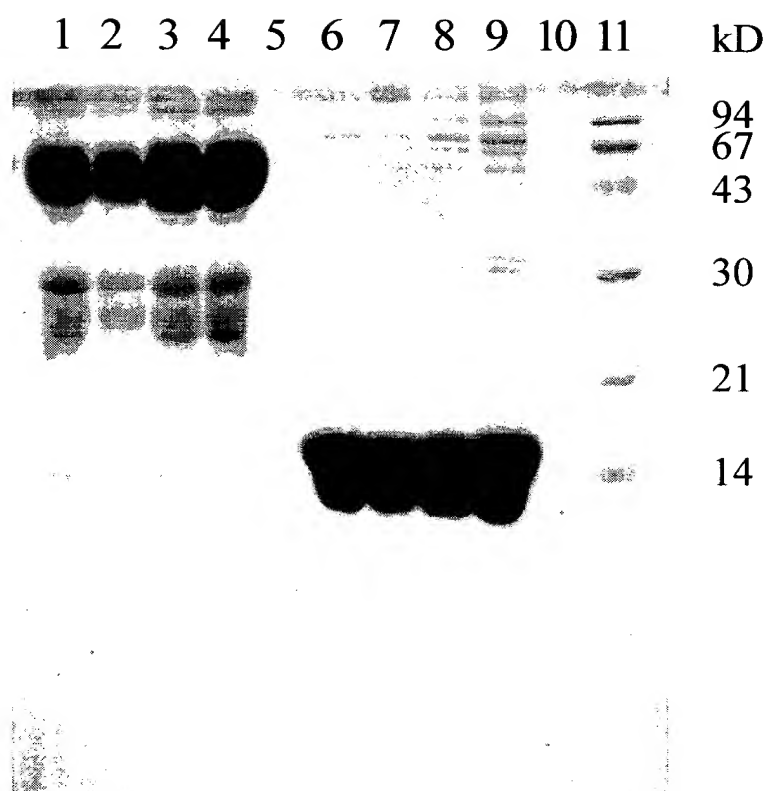


Fig. 2.2

09876543.012302

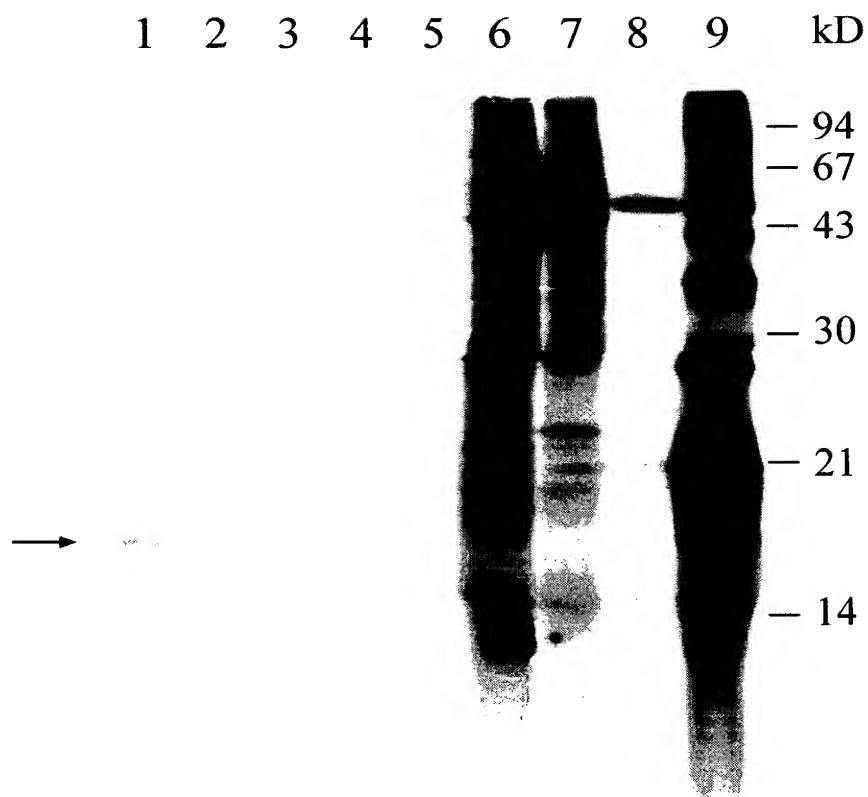


Fig. 2.3

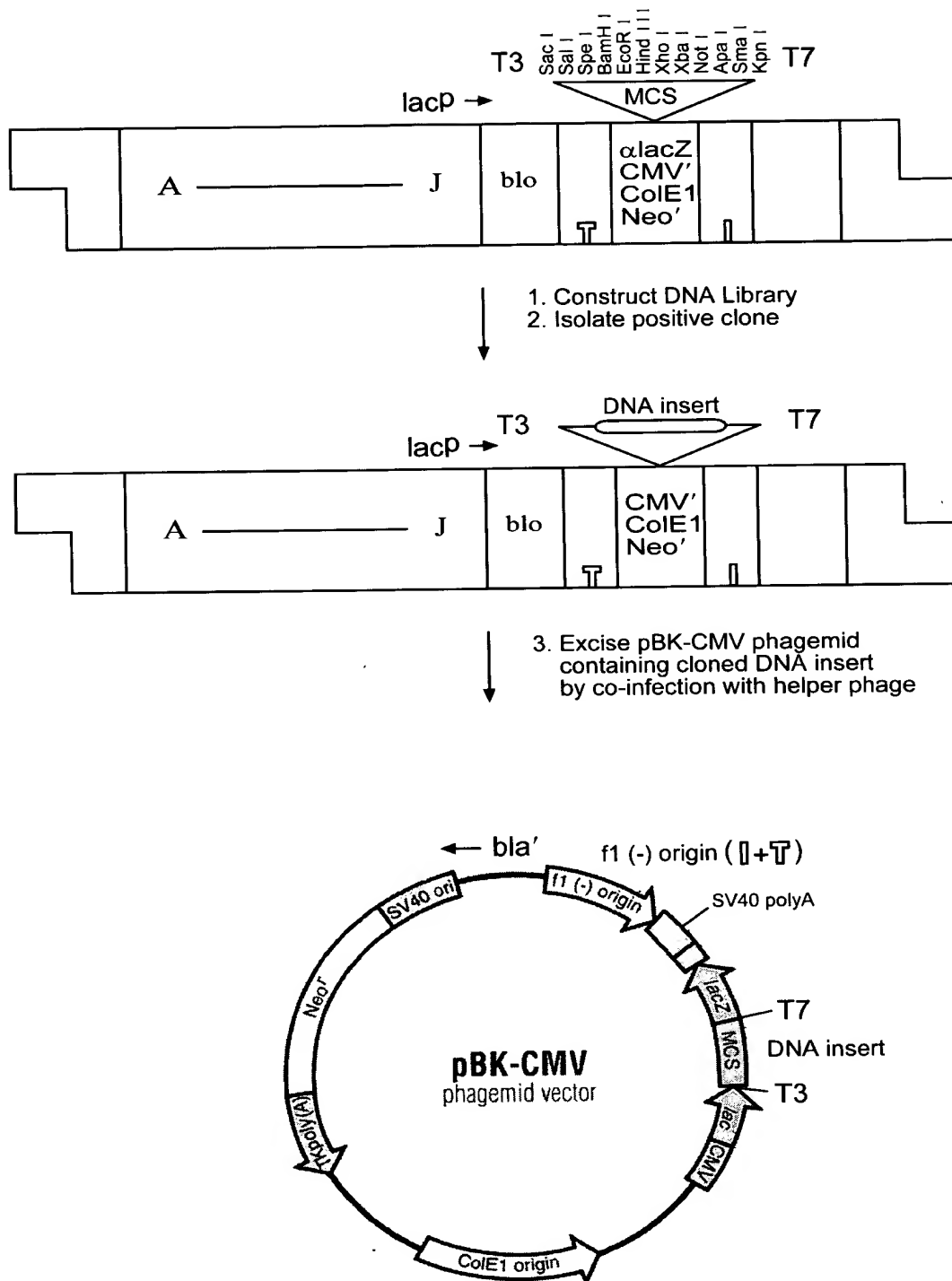


Fig. 2.4a

pBK-CMV
4518 bp

Restriction sites and features (clockwise from top):

- Ssp I 4410
- Nae I 134
- Ssp I 445
- Mlu I 463
- SV40 poly(A)
- SV40 3' splice
- T7 5' splice
- Kpn I 1019
- Sac I 1126
- T3
- Nhe I 1300
- Nsi I 1900
- CofE1 origin
- Mst II 2756
- Mst II 4388
- Nsi I 4303
- Nsi I 4231
- SV40 ori
- bla^P

Fig 2.4b

09252860

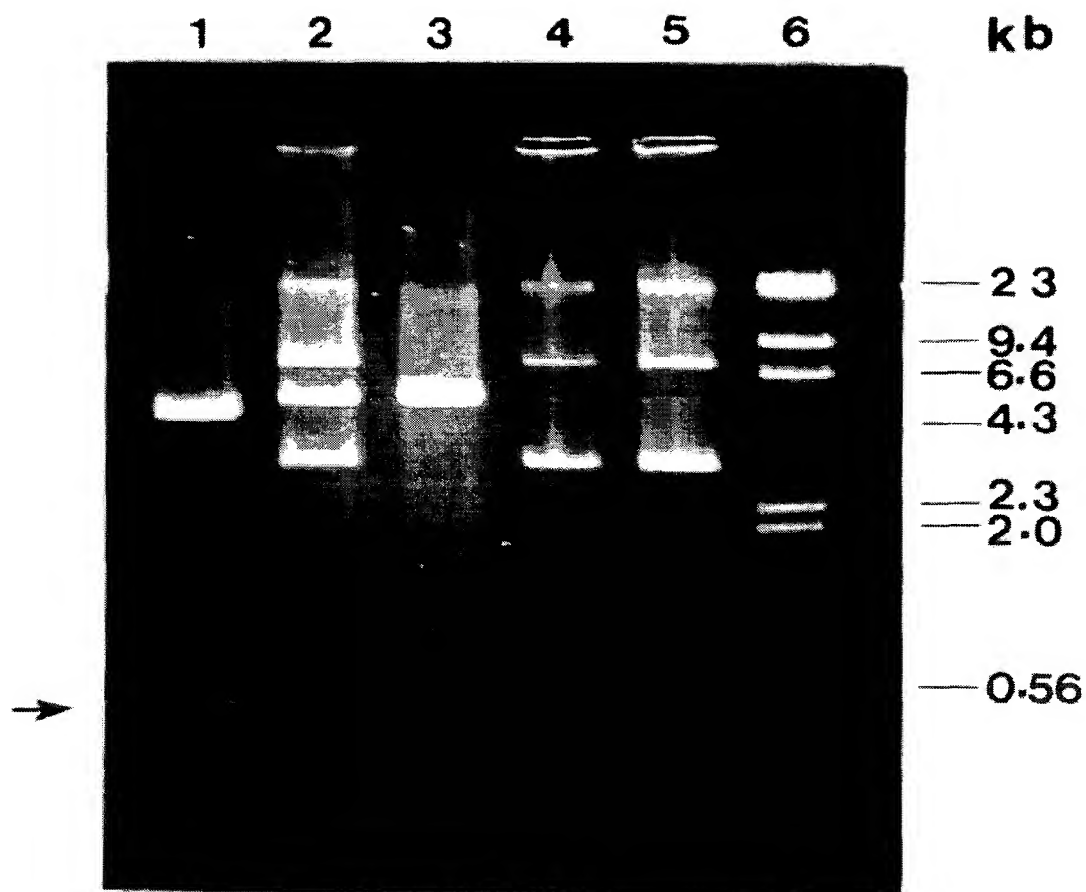


Fig. 2.5

COBETD" 88E32860

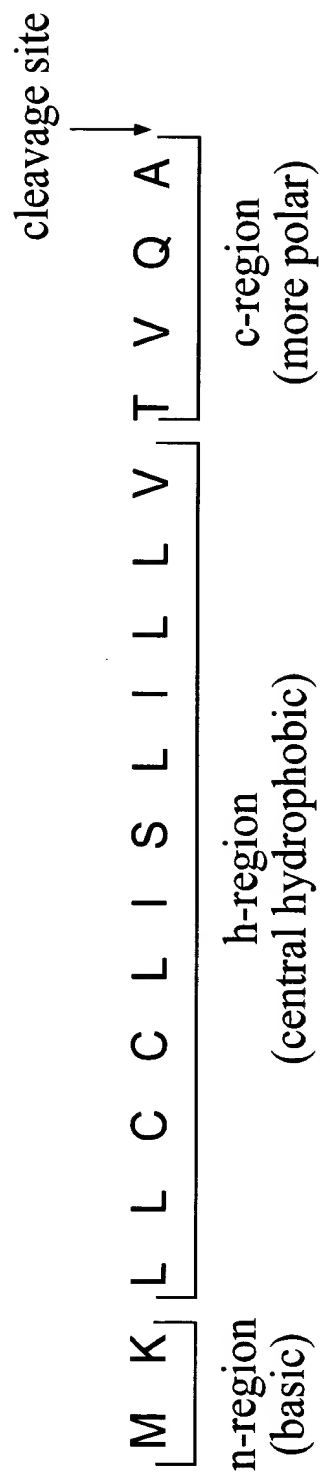


Fig. 2.6b

A. Mature Tm 13.17 amino acid residue

1 LTEAQIEKLN KISKKCQNES GVSQEIIITKA RNGDWEDDPK LKRQVFCVAR
 51 NAGLATESGE VVVDVLREKV RKVTDNDEET EKIINKCAVK RDTVEETVFN
 101 TFKCVMKNKP KFSPVD

B. Summary of the composition analysis for the mature Tm 13.17 sequence:

<u>Residue</u>	<u>Number</u>	<u>Mole Percent</u>
A = Ala	6	5.172
B = Asx	0	0.000
C = Cys	4	3.448
D = Asp	8	6.897
E = Glu	13	11.207
F = Phe	4	3.448
G = Gly	4	3.448
H = His	0	0.000
I = Ile	6	5.172
K = Lys	16	13.793
L = Leu	5	4.310
M = Met	1	0.862
N = Asn	8	6.897
P = Pro	3	2.586
Q = Gln	4	3.448
R = Arg	6	5.172
S = Ser	5	4.310
T = Thr	8	6.897
V = Val	14	12.069
W = Trp	1	0.862
Y = Tyr	0	0.000
Z = Glx	0	0.000

Molecular weight = 13171.96; Residues = 116; Average Residue Weight = 113.551

Charge = 1; Isoelectric point = 7.74.

Fig. 2.6c

2025-10-01 10:00:00

1	AOTGOATCCAAAGAAATTCGOCACGAGACTACTAAGATGAA	Tm 13.17 B 1
41 1	<div> <div>OTTGCTCTCTTTCT</div> <div>CTAATCTCTCTCATTTCTGTTOOTCA</div> <div>CTTACTTCTCTCATTTCTGTTOOTCC</div> </div>	Tm 13.17 B 1
81 28	<div> <div>OTTCAOCCCTT</div> <div>TAACCOAODCA</div> <div>CAAAATTOA</div> <div>AAACTOAA</div> <div>CA</div> </div>	Tm 13.17 B 1
121 68	<div> <div>AAATCAOC</div> <div>AAAAATOT</div> <div>CAAAAT</div> <div>TOAAAGT</div> <div>GOAOTOT</div> <div>CC</div> </div>	Tm 13.17 B 1
161 118	<div> <div>AAATCATRA</div> <div>CCAAAGCTC</div> <div>CCAA</div> <div>COOTGACT</div> <div>GGGAGGAC</div> </div>	Tm 13.17 B 1
201 148	<div> <div>ATCCCTAAACT</div> <div>TOAAA</div> <div>COCCAA</div> <div>OTTT</div> <div>TTTG</div> <div>CO</div> <div>TOGCC</div> <div>CA</div> <div>GA</div> </div>	Tm 13.17 B 1
241 188	<div> <div>ACGC</div> <div>COOTCT</div> <div>GGC</div> <div>CA</div> <div>COGAATC</div> <div>GOGA</div> <div>GO</div> <div>TO</div> <div>GGT</div> <div>TC</div> <div>GA</div> </div>	Tm 13.17 B 1
281 228	<div> <div>CO</div> <div>TTTT</div> <div>GA</div> <div>GGAGAG</div> <div>GTGA</div> <div>GA</div> <div>GA</div> <div>OOT</div> <div>CACT</div> <div>GA</div> <div>CA</div> <div>CA</div> <div>CA</div> <div>CA</div> </div>	Tm 13.17 B 1
321 268	<div> <div>GAAGAA</div> <div>CACT</div> <div>GAAGAA</div> <div>AAAT</div> <div>CACT</div> <div>CAAT</div> <div>TAAGTG</div> <div>CC</div> <div>CO</div> <div>CT</div> <div>CA</div> <div>GA</div> </div>	Tm 13.17 B 1
361 308	<div> <div>GA</div> <div>AT</div> <div>ACT</div> <div>GT</div> <div>TAAG</div> <div>GA</div> <div>AC</div> <div>GG</div> <div>GT</div> <div>TT</div> <div>CA</div> <div>AT</div> <div>ACT</div> <div>TT</div> <div>CA</div> <div>AA</div> <div>AT</div> </div>	Tm 13.17 B 1
401 348	<div> <div>TOT</div> <div>CAT</div> <div>TO</div> <div>AA</div> <div>AA</div> <div>AC</div> <div>AA</div> <div>OC</div> <div>CA</div> <div>AA</div> <div>OT</div> <div>TT</div> <div>CT</div> <div>CAC</div> <div>CA</div> <div>GT</div> <div>GA</div> <div>TT</div> <div>GA</div> </div>	Tm 13.17 B 1
441 388	<div> <div>ACC</div> <div>ACC</div> <div>ACC</div> <div>AC</div> <div>TA</div> <div>AG</div> <div>AT</div> <div>GG</div> <div>TT</div> <div>CA</div> <div>AA</div> <div>TO</div> <div>OT</div> <div>GT</div> <div>GC</div> <div>TT</div> <div>AC</div> </div>	Tm 13.17 B 1
481 428	<div> <div>AT</div> <div>AT</div> <div>AA</div> <div>AA</div> <div>AA</div> <div>AT</div> <div>GT</div> <div>TT</div> <div>CT</div> <div>GA</div> <div>TA</div> <div>TA</div> <div>AA</div> <div>AA</div> <div>AA</div> <div>AA</div> <div>AA</div> <div>AA</div> <div>AA</div> <div>AA</div> </div>	Tm 13.17 B 1

Fig. 2.7

Tm 13.17	3	EAQIEKLNKISKKCQNESGVSQEIITKARNGDWEDDPKLKRQVFCVARNA	52
	 : :. . : :. : :.	
AFP-3	1	ETPREKLKQHSDACKAESGVSEESLNKVRNREEVDDPKLKEHAF CILKRA	50
Tm 13.17	53	GLATESGEVVVDVLREKVRKVTDNDEETEKIINKCAVKRDTVEETVFNTF	102
		: .. . : :.. ... :.. ...:.. ...:.. ...:.. ...:..	
AFP-3	51	GFIDASGEFQLDHIKTKFKENSEHPEKVDDLVAKCAVKKDT PQHSSADFF	100
Tm 13.17	103	KCVMKNKP	110
		. :.	
AFP-3	101	KCVHDNRS	108

Percent identity: 39.8 (identical amino acids; Percent similarity: 58.3 (identical amino acids plus conservative amino acids).

Fig. 2.8

Tm 13.17	M	K	L	L	C	C	L	I	S	L	I	L	V	T	V	Q	A
AFP-3	M	K	L	L	L	C	L	V	L	V	A	L	V	A	T	Y	A
B Protein				L	T	S	L	I	L	L	V	A	V	Q	A		

Fig. 2.9

208270" 84E92B5D

Tm 13.17	NH2-L T	E A	Q I	E I	L N	K I S K	K C	Q N E
		:	:	:				
Tm 12.86	NH2-L T	D E	Q I	Q I	R N	K I S K	? Q	Q V

Fig 2.10

09876543210

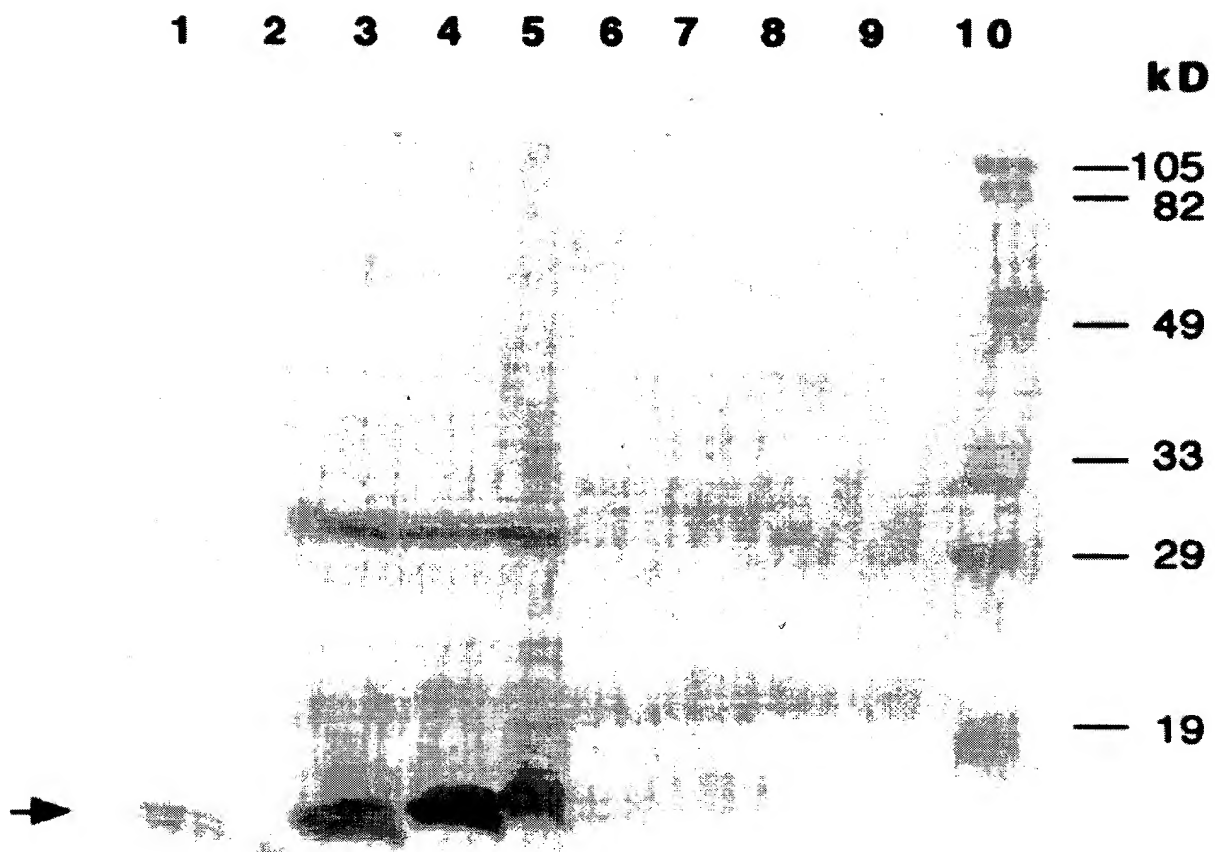


Fig 2.11

Tm 12.86 L T D E Q I Q K R N K I S K E ? Q Q V
 Tm 13.17 1 L T E A Q I E K L N K I S K K C Q N E S G V S Q E I I T K A
 B1 13 I T E E D L E L L R Q T S A E C K T E S G V S E D V I K R A
 AFP-3 1 E T P R E K L K Q H S D A C K A E S G V S E E S L N K V

Tm13.17 31 R N G D W E D D P K L K R Q V F C V A R N A G L A T E S G E
 B1 44 R K G D L E D D P K L K M Q L L C I F K A L E I V A E S G E
 AFP-3 29 R N R E E V D D P K L K E H A F C I L K R A G F I D A S G E

Tm13.17 61 V V V D V L R E K V R K V T D N D E E T E K I I N K C A V K
 B1 75 I E A D T F K E K L T R V T N D D E E S E K I V E K C T V T
 AFP-3 59 F Q L D H I K T K F K E N S E H P E K V D D L V A K C A V K

Tm13.17 91 R D T V E E T V F N T F K C V M K N K P K F S P V D
 B1 106 E D T P E D T A F E V T K C V L K D K P N F F G D L F V
 AFP-3 89 K D T P Q H S S A D F F K C V H D N R S

Fig. 2.12

polyadenylation signal

poly (A) tail

Fig. 3.0

1 GGCACGAGCAAAA ATGAAACTCCTCTTGTGCTTTGCTTTGCGCGCC
M K L L L C F A F A A

47 ATCGTCATCGGAGCTCAGGCTCTCACCGACGAACAGATACAGAAA
I V I G A Q A L T D E Q I Q K

92 AGGAACAAGATCAGCAAAGAATGCCAGCAGGTGTCCGGAGTGTCC
R N K I S K E C Q Q V S G V S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGACGAT
Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAAAGCACGTCTCTGCTTCTCGAAGAAAAGTGGAA
P K M K K H V L C F S K K T G

226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAAGTGGACAAGATCGTG
K L K H V A S D E E V D K I V

316 CAGAAGTGCGTGGTCAAGAAGGCCACACCAGAGGAAACGGCTTAT
Q K C V V K K A T P E E T A Y

361 GACACCTTCAAGTGTATTTACGACAGTAAACCTGATTTCTCTCCT
D T F K C I Y D S K P D F S P

406 ATTGATTAAATTGTTTTGTATTTGACTGAATTTTGACAATAAAGGT
I D

451 ACTATCGTTATGAAAAAAAAAAAAAAAAAAAAA

polyadenylation signal

poly (A) tail

Fig 3.1

Start
↓

2-2	G G C A C G A G C A A A A A T G A A A C T C C T C T T G T G C T T T T G C G
2-3	G G C A C G A G C A A A A A T G A A A C T C C T C T T G T G C T T T T G C T
2-2	T T C G C C G C C A T C G T C A T C G G A G C T C A G G C T C T C A C C G
2-3	T T C G C C G C C A T C G T C A T C G G A G C T C A G G C T C T C A C C G
2-2	A C G A A C A G A T A C A G A A A A G G A A C A A G A T C A G C A A A G A
2-3	A C G A A C A G A T A C A G A A A A G G A A C A A G A T C A G C A A A G A
2-2	A T G C C A G C A G G T G T C C G G A G T G T C C C A A G A G A C G A T C
2-3	A T G C C A G C A G G T G T C C G G A G T G T C C C A A G A G A C G A T C
2-2	G A C A A A G T C C G C A C A G G T G T C T T G G T C G A T G A T C C C A
2-3	G A C A A A G T C C G C A C A G G T G T C T T G G T C G A C G A T C C C A
2-2	A A A T G A A G A A G C A C G T C C T C T G C T T C T C G A A G A A A A C
2-3	A A A T G A A G A A G C A C G T C C T C T G C T T C T C G A A G A A A A C
2-2	T G G A G T G G C A A C C G A A G C C G G A G A C A C C A A T G T G G A G
2-3	T G G A G T G G C A A C C G A A G C C G G A G A C A C C A A T G T G G A G
2-2	G T A C T C A A A G C C A A G C T G A A G C A T G T G G C C A G C G A C G
2-3	G T A C T C A A A G C C A A G C T G A A G C A T G T G G C C A G C G A C G
2-2	A A G A G G T G G A C A A G A T C G T G C A G A A G T G C G T G G T C A A
2-3	A A G A A G T G G A C A A G A T C G T G C A G A A G T G C G T G G T C A A
2-2	G A A G G C C A C A C C A G A G G A A A C G G C T T A T G A C A C C T T C
2-3	G A A G G C C A C A C C A G A G G A A A C G G C T T A T G A C A C C T T C
2-2	A A G T G T A T T T A C G A C A G C A A A C C T G A T T T C T C T C C T A
2-3	A A G T G T A T T T A C G A C A G T A A A C C T G A T T T C T C T C C T A
2-2	T T G A T T A A T T G T T T T G T A T T T G A C T G A A T T T T G A C A A
2-3	T T G A T T A A T T G T T T T G T A T T T G A C T G A A T T T T G A C A A
2-2	T A A A G G T A A T A T C G T T A T G T A A A A A
2-3	T A A A G G T A C T A T C G T T A T G A A A A A A

Fig 3.2

Predicted Amino Acid

Composition of 2-2 and 2-3

Analysis	Whole Protein
Molecular Weight	12843.80 m.w.
Length	115
1 microgram =	77.859 pMoles
Molar Extinction coefficient	3040±5%
1 A(280) =	4.22 mg/ml
Isoelectric Point	7.11
Charge at pH 7	0.13

Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	48	47.19	41.74
Acidic (DE)	20	18.90	17.39
Basic (KR)	20	20.40	17.39
Polar (NCQSTY)	30	25.35	26.09
Hydrophobic (AILFWV)	34	27.26	29.57
A Ala	6	3.32	5.22
C Cys	4	3.21	3.48
D Asp	11	9.86	9.57
E Glu	9	9.05	7.83
F Phe	3	3.44	2.61
G Gly	4	1.78	3.48
H His	2	2.14	1.74
I Ile	6	5.29	5.22
K Lys	18	17.97	15.65
L Leu	5	4.41	4.35
M Met	1	1.02	0.87
N Asn	2	1.78	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.98	5.22
R Arg	2	2.43	1.74
S Ser	7	4.75	6.09
T Thr	9	7.08	7.83
V Val	14	10.80	12.17
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
. Ter	0	0.00	0.00

Fig. 3.3

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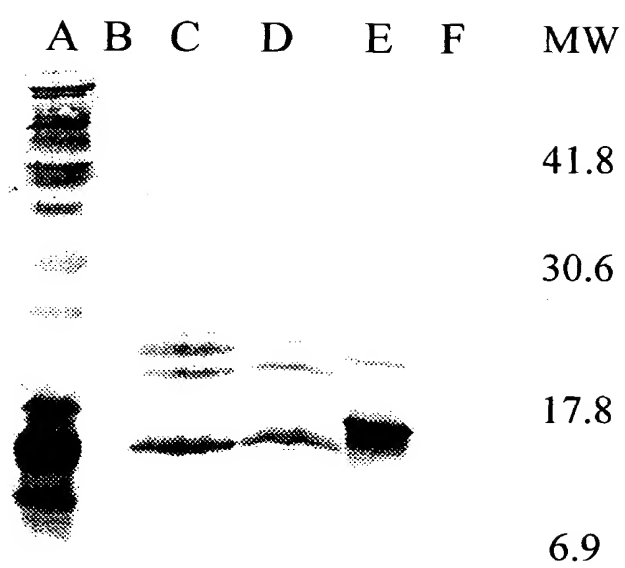


Fig. 3.4

0097549 012000

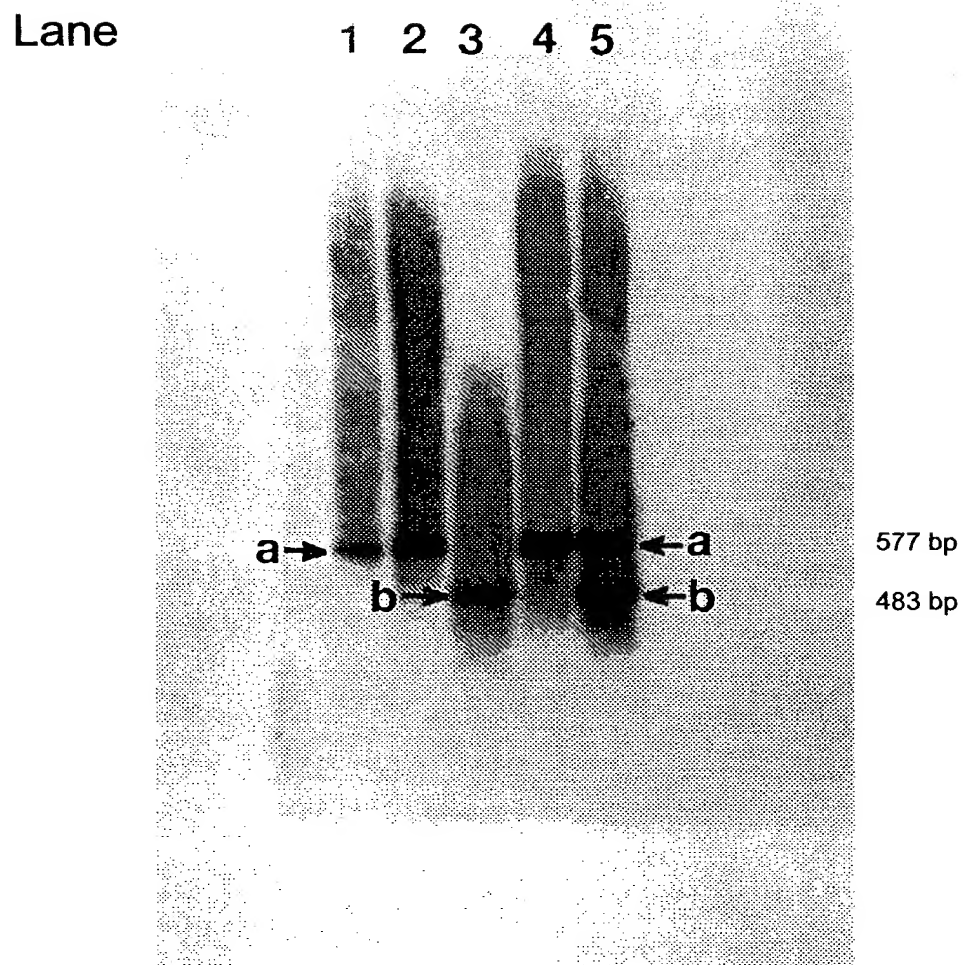


Fig. 4.0

09876543210

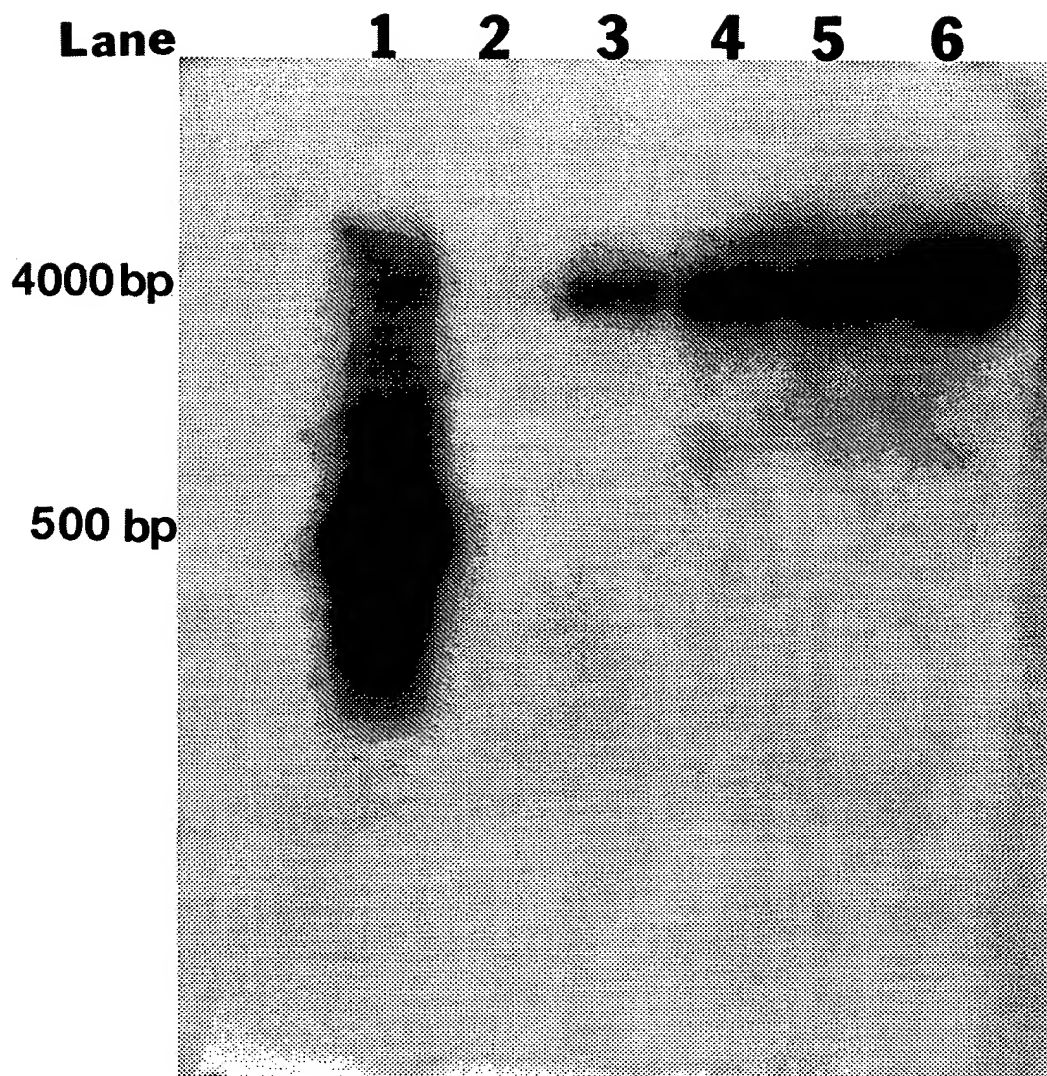


Fig. 4.1

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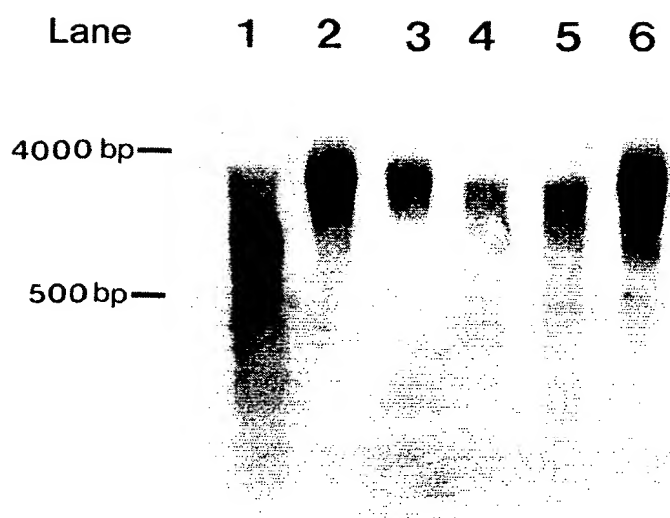
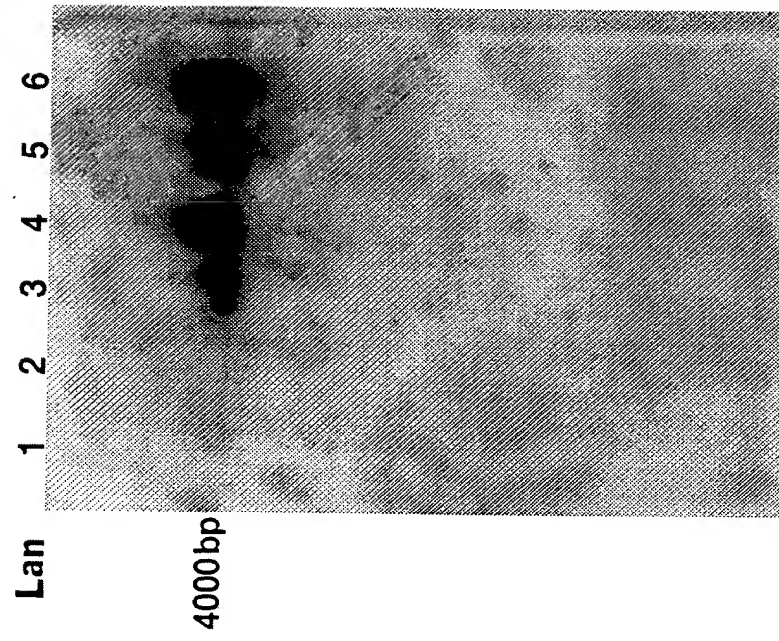


Fig. 4.2

A.



B.

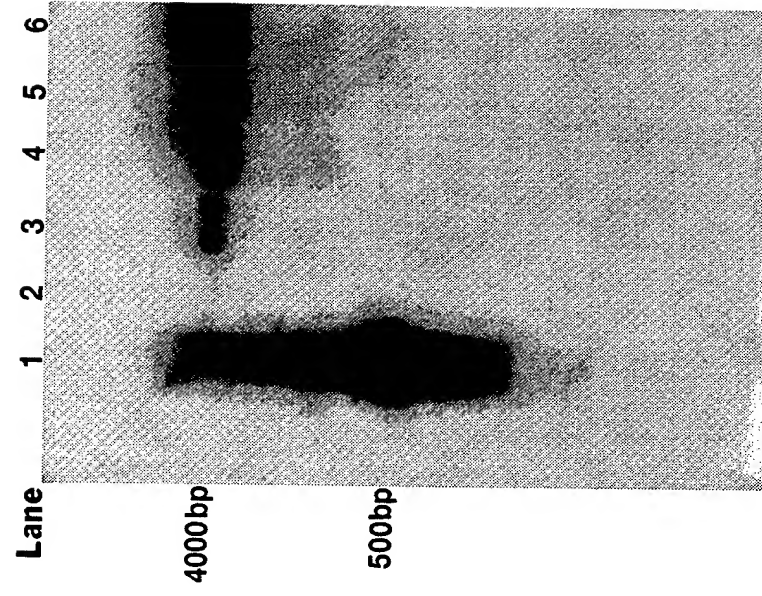


Fig. 4.3

09875349, 042882

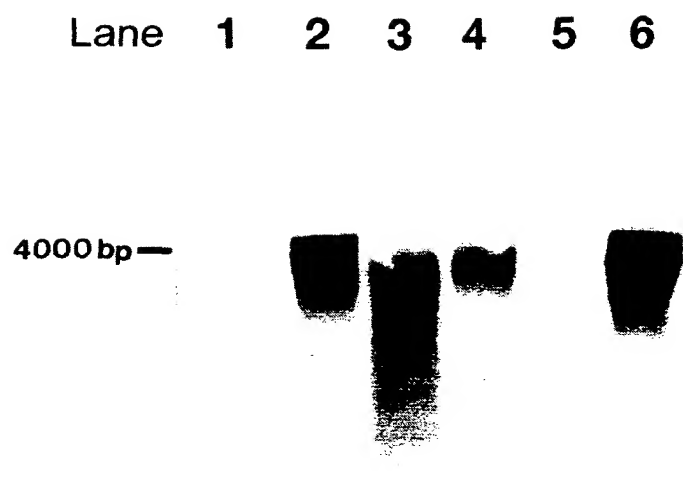
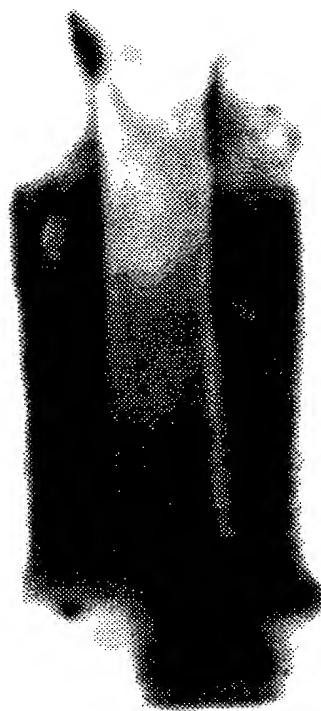


Fig. 4.4

09876543 012345

Lane 1 2 3 4 5



23130

9416

4361

2322

2027

564

Fig. 4.5

Tm 13.17 cDNA

1 AGTGGATCCAAAGAATTTCGGCACGAGACTACTAAGATGAGTTGCTCTGTTGTCTAATCT
M K L L C C L I S

61 CCCTCATTCTGTTGGTCACAGTTCAGGCCCTGACCGAGGCACAAATTGAGAACTGAACA
L I L L V T V Q A L T E A Q I E K L N K
↑ Forward Primer

121 AGATCAGCAAAAAATGTCAAATGAAAGTGGAGTGTCTCGCAAGAGATCATAACCAAAGCTC
I S K K C Q N E S G V S Q E I I T K A R

181 GCAACGGTGAAGTGGGAGGACGATCCTAACTGAAACGCCAAGTTTTTTGCGTGGCCAGGA
N G D W E D D P K L K R Q V F C V A R N

241 ACGCCGGTCTGGCCACGGAATCGGGAGAGGTGGTGGTTCGACGTGTTGAGGGAGAAGGTGA
A G L A T E S G E V V V D V L R E K V R

301 GGAAGGTCACTGACAACGACGAAGAACTGAGAAAATCATCAATAAGTGCGCCGTCAAGA
K V T D N D E E T E K I I N K C A V K R
Reverse Primer

361 GAGATACTGTTGAAGAGACGGTGTTCATACTTTCAAATGTGTCATGAAAAACAAGCCAA
D T V E E T V F N T F K C V M K N K P K

421 AGTTCTCACCAGTTGATTGAACCACCACGACTAGTAGATGGTTCAAATGGTGTGCTTTAC
F S P V D *

481 ATATAAAAAATAAAGTGTCTGATGTAAAAAATAAAAAAAAAAAAAAAAAAACTCG
polyadenylation signal poly (A) tail (26)

537 AGAGTATTCTAGAGCGGCCCGGGCCCATCGTTTCCACCC

Fig. 4.6a

Forward Primer

2-2 L T D E Q I Q K R N K I S K E C Q Q V S G V S Q E T I D K V R T G V L V
T_m 13.17 L T E A Q I E K L N K I S K K C O N E S G V S Q E I I T K A R N G D W E
B2 L T E E D L Q L L R Q T S A E C K T E S G A S E A V I K K A R K G D L E
AFP-3 E T P R E K L K Q H S D A C K A E S G V S E E S L N K V R N R E E V

2-2 D D P K M K K H V L C F S K K T G V A T E A G D T N V E V L K A K L K H
T_m 13.17 D D P K L K R Q V F C V A R N A G L A T E S G E V V V D V L R E K V R K
B2 D D P K L K M Q L L C I F K A L E I V A E S G E I E A D T F K E K L T R
AFP-3 D D P K L K E H A F C I L K R A G F I D A S G E F Q L D H I K T K F K E

Reverse Primer

2-2 V A S D E E V D K I V Q K C V V K K A T P E E T A Y D T F K C I Y D S
T_m 13.17 V T D N D E E T E K I I N K C A V K R D T V E E T V F N T F K C V M K N
B2 V T N D D E E S E K I V E K C T V T E D T P E D T A F E V T K C V L K D
AFP-3 N S E H P E K V D D L V A K C A V K K D T P Q H S S A D F F K C V H D N

2-2 K P D F S P I D
T_m 13.17 K P K F S P V D
B2 K P N F F G D L F V
AFP-3 R S

Fig. 4.6b

Primer	percent % composition				Melting Temperature (°C)
	A	C	G	T	
Forward	28.6	14.3	42.9	14.3	44.0
Reverse	25.0	31.3	6.3	37.5	44.0

Fig. 4.6c

09876349.012803

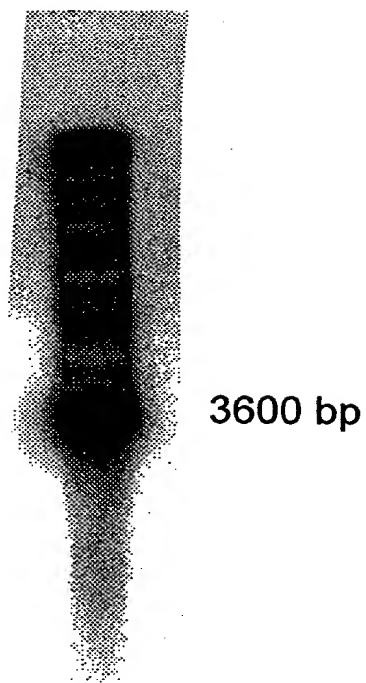


Fig. 4.7

0975348-012003

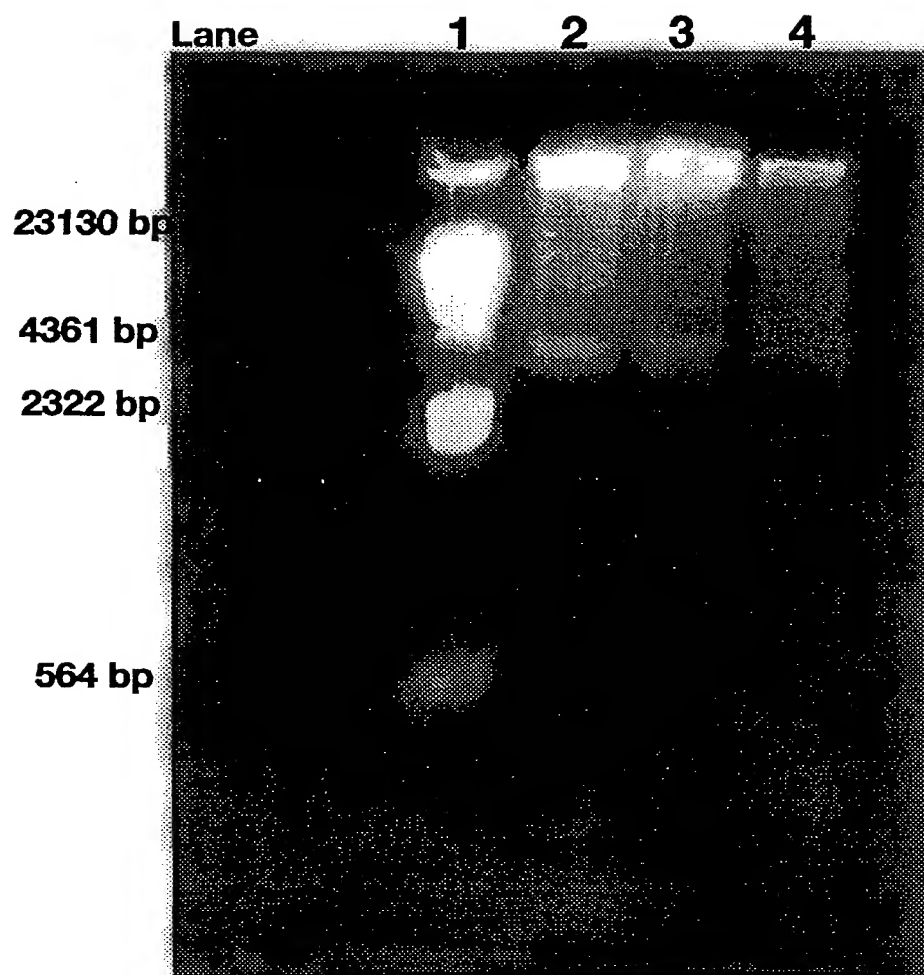


Fig. 4.8

0907E348.012802

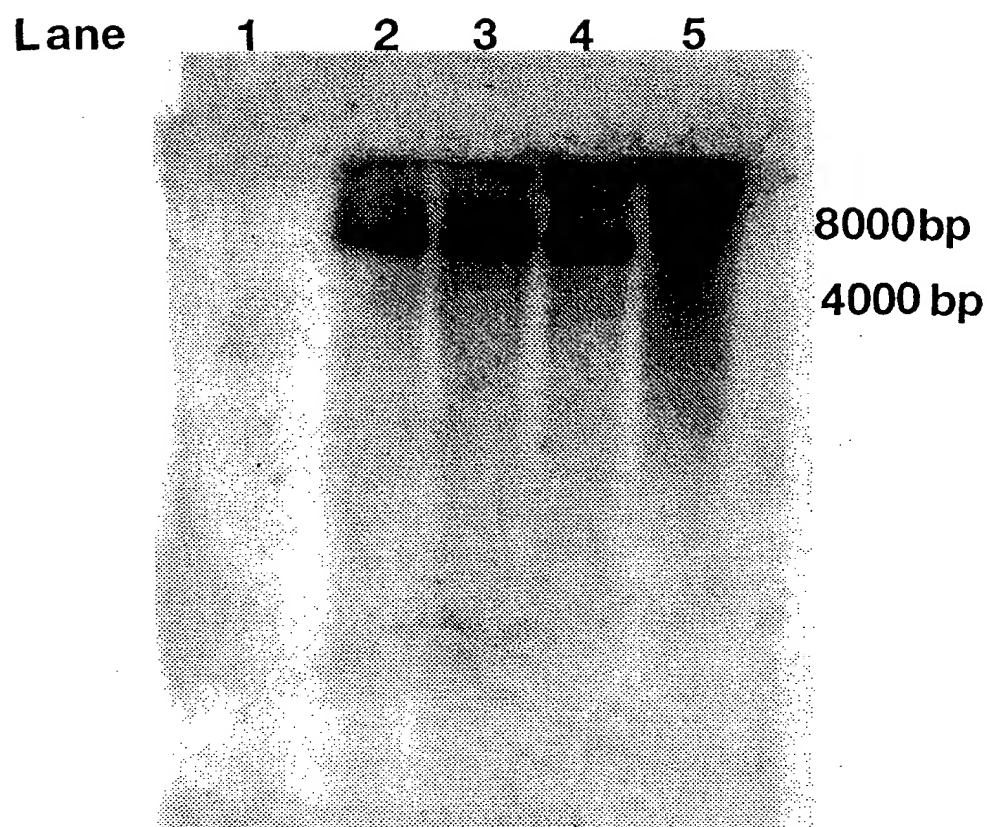


Fig. 4.9

1 GGCACGAGCAAAA ATGAAACTCCTCTTGTGCTTTGCTTTGCGCGCC
M K L L L C F A F A A

47 ATCGTCATCGGAGCTCAGGCTCTCACCGACGAACAGATACAGAAA
I V I G A Q A L T D E Q I Q K

92 AGGAACAAGATCAGCAAAGAATGCCAGCAGGTGTCCGGAGTGTCC
R N K I S K E C Q Q V S G V S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGACGAT
Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAAAACCTGGA
P K M K K H V L C F S K K T G

226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAGGTGGACAAGATCGTG
K L K H V A S D E E V D K I V

316 CAGAAGTGCGTGGTCAAGAAGGCCACACCAGAGGAAACGGCTTAT
Q K C V V K K A T P E E T A Y

361 GACACCTTCAAGGTTATTTACGACAGTAAACCTGATTTCTCTCCT
D T F K V I Y D S K P D F S P

406 ATTGATTAATTGTTTTGTATTTGACTGAATTTTGACAATAAAGGT
I D .

451 ACTATCGTTATGTAAAAAAAAAAAAAAAAAAAAA polyadenylation signal

poly (A) tail

Fig. 4.10a

Predicted Amino Acid

Composition of 3-4

Molecular Weight	12839.70 m.w.
Length	115
1 microgram =	77.883 pMoles
Molar Extinction coefficient	2920±5%
1 A(280) =	4.40 mg/ml
Isoelectric Point	7.14
Charge at pH 7	0.16

Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	47	46.41	40.87
Acidic (DE)	20	18.91	17.39
Basic (KR)	20	20.41	17.39
Polar (NCQSTY)	29	24.55	25.22
Hydrophobic (AILFWV)	35	28.04	30.43
A Ala	6	3.32	5.22
C Cys	3	2.41	2.61
D Asp	11	9.86	9.57
E Glu	9	9.05	7.83
F Phe	3	3.44	2.61
G Gly	4	1.78	3.48
H His	2	2.14	1.74
I Ile	6	5.29	5.22
K Lys	18	17.97	15.65
L Leu	5	4.41	4.35
M Met	1	1.02	0.87
N Asn	2	1.78	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.99	5.22
R Arg	2	2.43	1.74
S Ser	7	4.75	6.09
T Thr	9	7.09	7.83
V Val	15	11.58	13.04
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
. Ter	0	0.00	0.00

Fig. 4.10b

1 GGCACGAGCAAAA ATGAAACTCCTCTTGTGCTTTGCTTTGCGCGCC
M K L L L C F A F A A

47 ATCGTCATCGGAGCTCAGGCTCTCACCGATGAACAGATACAGAAA
I V I G A Q A L T D E Q I Q K

92 AGGAACAAGATCAGCAAAGAATGCCAGCAGGAGTCCGGAGTGTCC
R N K I S K E C Q Q E S G V S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGACGAT
Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAGAACTGGA
P K M K K H V L C F S K R T G

226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTA CTCAAAGCC
V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAAGTGGACAAGATCGTG
K L K H V A S D E E V D K I V

316 CAGAAGTGCGTGGTCAAGAAGGCCACACCAGAGGAAACGGCTTAT
Q K C V V K K A T P E E T A Y

361 GACACCTTCAAGTGTATTTACGACAGTAAACCTGATTTCTCTCCT
D T F K V I Y D S K P D F S P

406 ATTGATTAATTGTTTTGTATTTGACTGAATTTTGACAATAAAGGT
I D

451 ACTATCGTTATGAAAAAAAAAAAAAAAAAAAAA

polyadenylation signal

poly (A) tail

Fig. 4.11a

Predicted Amino Acid

Composition of 3-9

Analysis	Whole Protein
Molecular Weight	12871.80 m.w.
Length	115
1 microgram =	77.689 pMoles
Molar Extinction coefficient	3040±5%
1 A(280) =	4.23 mg/ml
Isoelectric Point	7.11
Charge at pH 7	0.13

Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	48	47.31	41.74
Acidic (DE)	20	18.86	17.39
Basic (KR)	20	20.57	17.39
Polar (NCQSTY)	30	25.29	26.09
Hydrophobic (AILFWV)	34	27.20	29.57
A Ala	6	3.31	5.22
C Cys	4	3.21	3.48
D Asp	11	9.84	9.57
E Glu	9	9.03	7.83
F Phe	3	3.43	2.61
G Gly	4	1.77	3.48
H His	2	2.13	1.74
I Ile	6	5.28	5.22
K Lys	17	16.93	14.78
L Leu	5	4.40	4.35
M Met	1	1.02	0.87
N Asn	2	1.77	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.97	5.22
R Arg	3	3.64	2.61
S Ser	7	4.74	6.09
T Thr	9	7.07	7.83
V Val	14	10.78	12.17
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
. Ter	0	0.00	0.00

Fig. 4.116

1 GGCACGAGCAAAAATGAAACTCCTCTTGTGCTTTGCGTTTCGCCGCC
M K L L L C F A F A A

47 ATCGTCATCGGAGCTCAGGCTCTCACCGACGAACAGATACAGAAA
I V I G A Q A L T D E Q I Q K

92 AGGAACAAGATCAGCAAAGAGTGCCAGCAGGTGTCCGGAGTGTCC
R N K I S K E C Q Q E S G V S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGACGAT
Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAAAAGTGGG
P K M K K H V L C F S K R T G

226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAAGTGGACAAGATCGTG
K L K H V A S D E E V D K I V

316 CAGAAGTGCGTGGTCAAGAAGGCCACACCAGAGGAAACGGCTTAT
Q K C V V K K A T P E E T A Y

361 GACACCTTCAAGTGTATTTACGACAGTAAACCTGATTTCTCTCCT
D T F K V I Y D S K P D F S P

406 ATTGATTAAATTGTTTTGTATTTGGCTGAATTTTGACAATAAAGGT
I D

451 ACTATCGTTATGTAAAAAAAAAAAAAAAAAAAAA

polyadenylation signal

poly (A) tail

Fig. 4.12a

Predicted Amino Acid

Composition of 7-5

Analysis	Whole Protein
Molecular Weight	12843.80 m.w.
Length	115
1 microgram =	77.859 pMoles
Molar Extinction coefficient	3040±5%
1 A(280) =	4.22 mg/ml
Isoelectric Point	7.11
Charge at pH 7	0.13

Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	48	47.19	41.74
Acidic (DE)	20	18.90	17.39
Basic (KR)	20	20.40	17.39
Polar (NCQSTY)	30	25.35	26.09
Hydrophobic (AILFWV)	34	27.26	29.57
A Ala	6	3.32	5.22
C Cys	4	3.21	3.48
D Asp	11	9.86	9.57
E Glu	9	9.05	7.83
F Phe	3	3.44	2.61
G Gly	4	1.78	3.48
H His	2	2.14	1.74
I Ile	6	5.29	5.22
K Lys	18	17.97	15.65
L Leu	5	4.41	4.35
M Met	1	1.02	0.87
N Asn	2	1.78	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.98	5.22
R Arg	2	2.43	1.74
S Ser	7	4.75	6.09
T Thr	9	7.08	7.83
V Val	14	10.80	12.17
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
. Ter	0	0.00	0.00

Fig. 4.12b

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[illegible]

220210* 01E34300

2-2 MK L L L C F A F A A I V I G A Q A L T D E Q I Q K R N K I S K E C Q Q V S G V S Q E T I D K V R T G V L V
2-3 MK L L L C F A F A A I V I G A Q A L T D E Q I Q K R N K I S K E C Q Q V S G V S Q E T I D K V R T G V L V
3-4 MK L L L C F A F A A I V I G A Q A L T D E Q I Q K R N K I S K E C Q Q V S G V S Q E T I D K V R T G V L V
3-9 MK L L L C F A F A A I V I G A Q A L T D E Q I Q K R N K I S K E C Q Q V S G V S Q E T I D K V R T G V L V
7-5 MK L L L C F A F A A I V I G A Q A L T D E Q I Q K R N K I S K E C Q Q V S G V S Q E T I D K V R T G V L V

2-2 D D P K M K K H V L C F S K K T G V A T E A G D T N V E V L K A K L K H V A S D E E V D D K I V Q K C V V K K
2-3 D D P K M K K H V L C F S K K T G V A T E A G D T N V E V L K A K L K H V A S D E E V D D K I V Q K C V V K K
3-4 D D P K M K K H V L C F S K K T G V A T E A G D T N V E V L K A K L K H V A S D E E V D D K I V Q K C V V K K
3-9 D D P K M K K H V L C F S K K T G V A T E A G D T N V E V L K A K L K H V A S D E E V D D K I V Q K C V V K K
7-5 D D P K M K K H V L C F S K K T G V A T E A G D T N V E V L K A K L K H V A S D E E V D D K I V Q K C V V K K

2-2 A T P E E T A Y D T F F K C I Y D S K P P D F S P I D *
2-3 A T P E E T A Y D T F F K C I Y D S K P P D F S P I D *
3-4 A T P E E T A Y D T F F K C I Y D S K P P D F S P I D *
3-9 A T P E E T A Y D T F F K C I Y D S K P P D F S P I D *
7-5 A T P E E T A Y D T F F K C I Y D S K P P D F S P I D *

Fig. 4.14

	MW	AA	Cys	Pro	Phe	Ile	Val	Met	Leu	% most hydrophobic	(% mole)										% most hydrophilic	
	(kDa)	(#)									Gly	Ala	Tyr	His	Trp	Asx	Glx	Arg	Lys	Ser	Thr	
Tm 12.86	12.86	117	3.2	3.0	3.4	4.4	8.5	2.0	4.4	28.9	3.1	3.9	3.8	3.2	ND	10.7	15.0	3.6	14.9	6.8	6.3	57.3
Tm 13.17	13.17	116	3.13	2.21	4.47	5.16	10.5	1.0	4.3	29.11	1.73	3.24	0	0	1.41	0	0	7.12	15.6	3.31	6.14	32.14
2-2	12.84	115	3.21	3.02	3.44	5.29	10.8	1.02	4.41	27.26	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.08	32.23
2-3	12.84	115	3.21	3.02	3.44	5.29	10.8	1.02	4.41	27.26	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.08	32.23
3-4	12.84	115	2.41	3.02	3.44	5.29	11.6	1.02	4.41	28.04	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.09	32.24
3-9	12.87	115	3.21	3.02	3.43	5.28	10.8	1.02	4.40	27.20	1.77	3.31	2.54	2.13	0	0	0	3.64	16.9	4.74	7.07	32.38
7-5	12.84	115	3.21	3.02	3.44	5.29	10.8	1.02	4.41	27.26	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.08	32.23

Fig. 4.15

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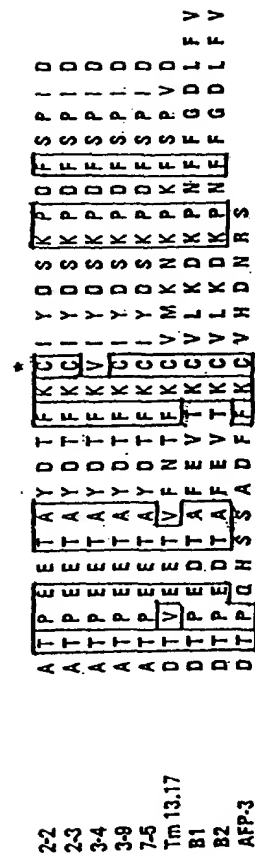
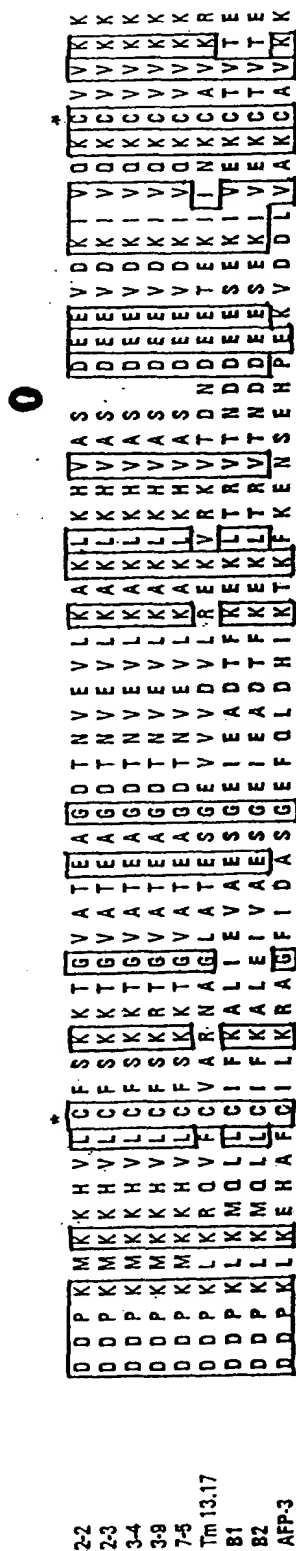
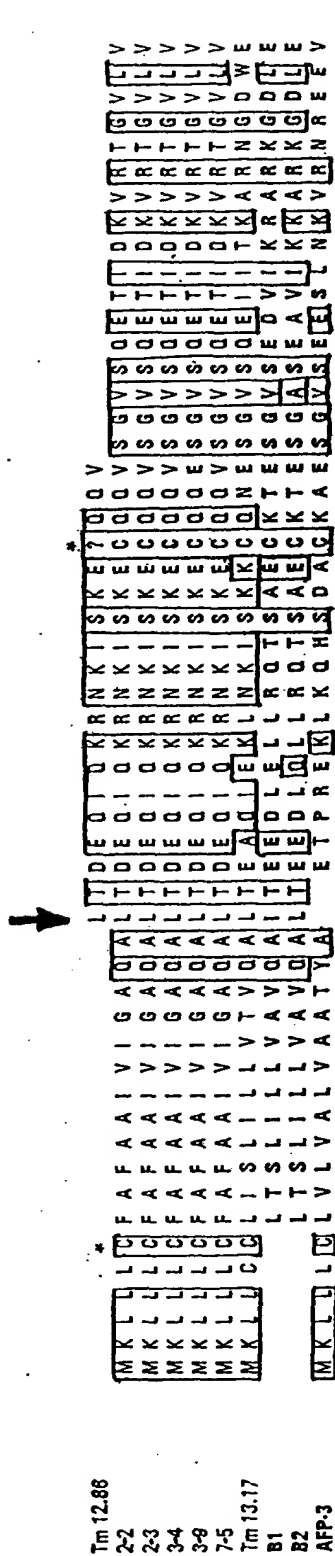


FIG 4.16
* = conserved cysteine (yellow)

Boxed = conserved residues in ≥ 7 Genes (blue or orange)

Fig. 4.16

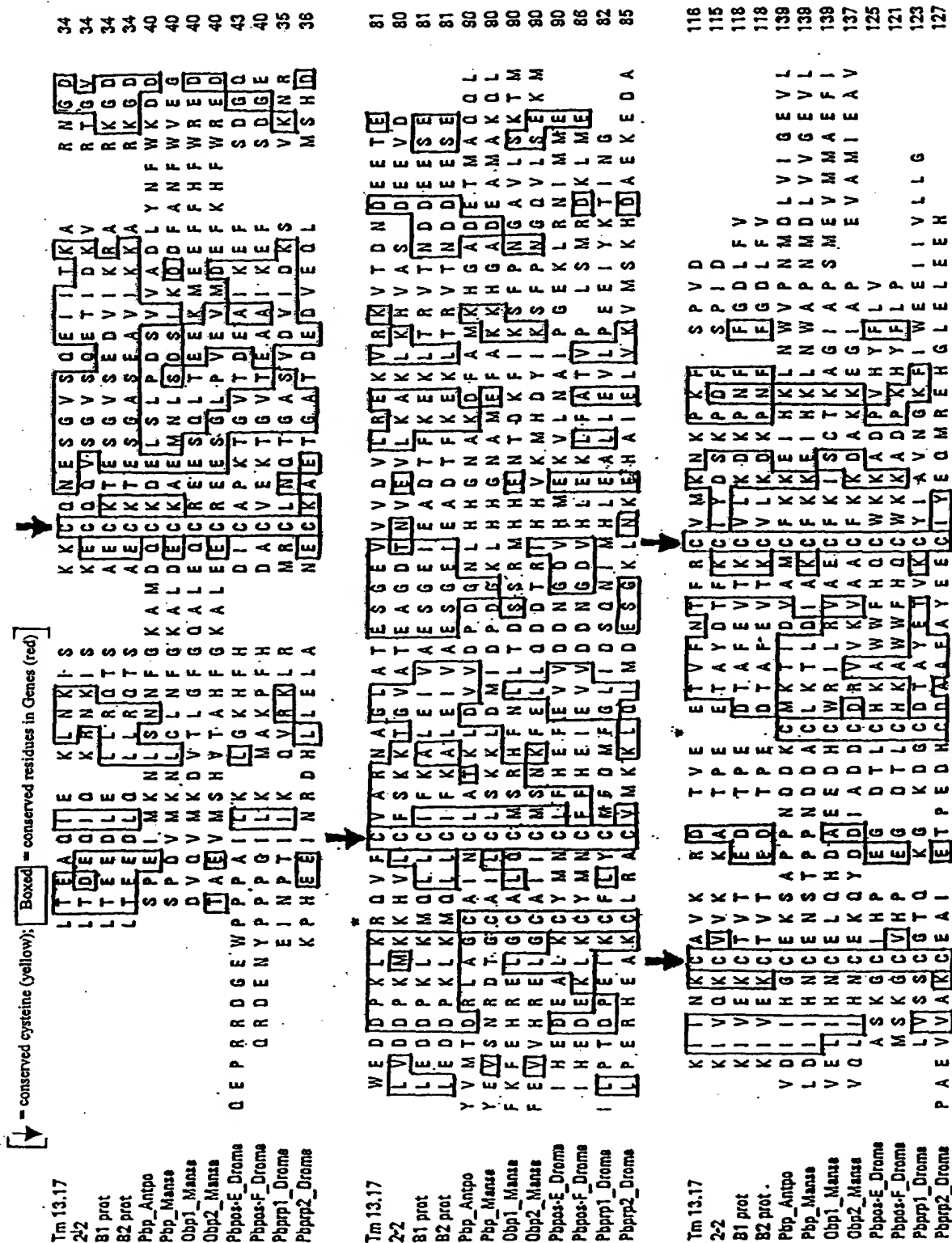
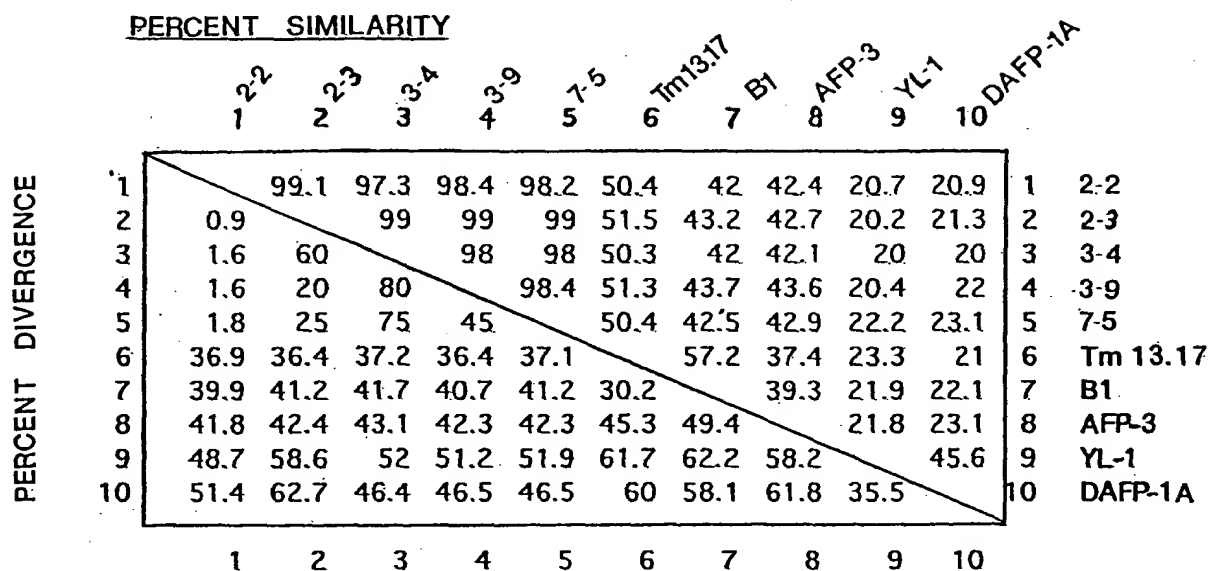


Fig. 4.17

NUCLEOTIDE SEQUENCES



AMINO ACID SEQUENCES

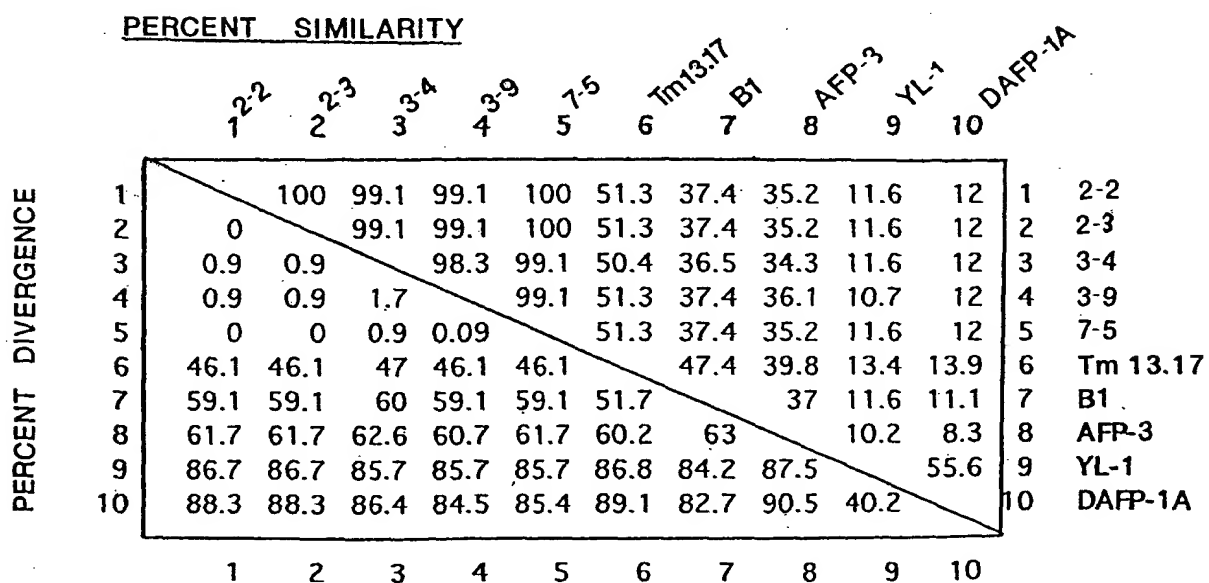


Fig. 4.19

203210" 84E92860

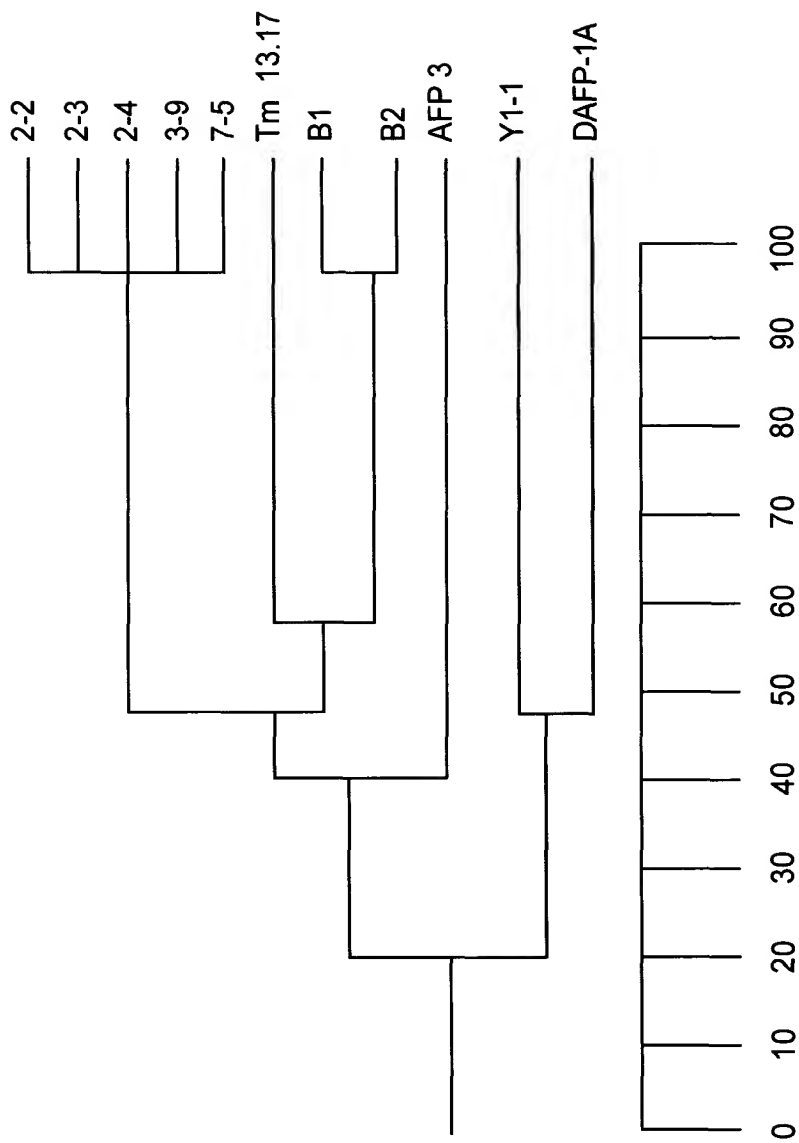


Fig. 4.20

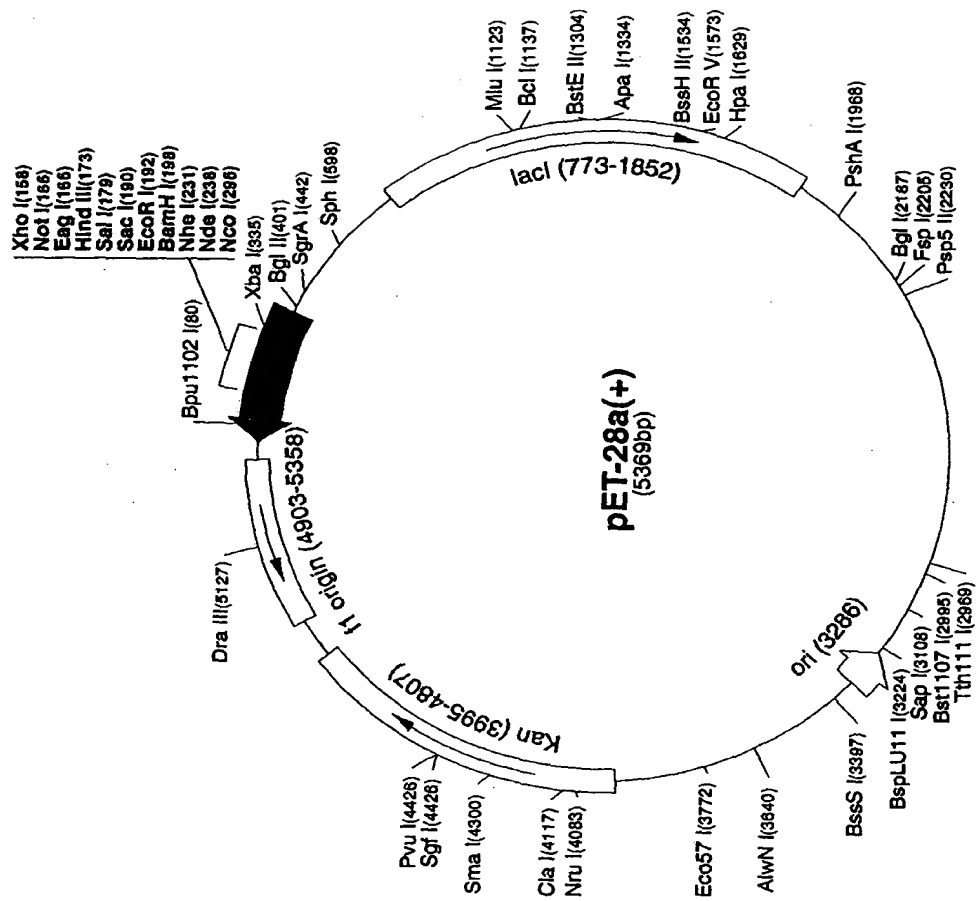


Fig. 5.0

200210" BHE3/360

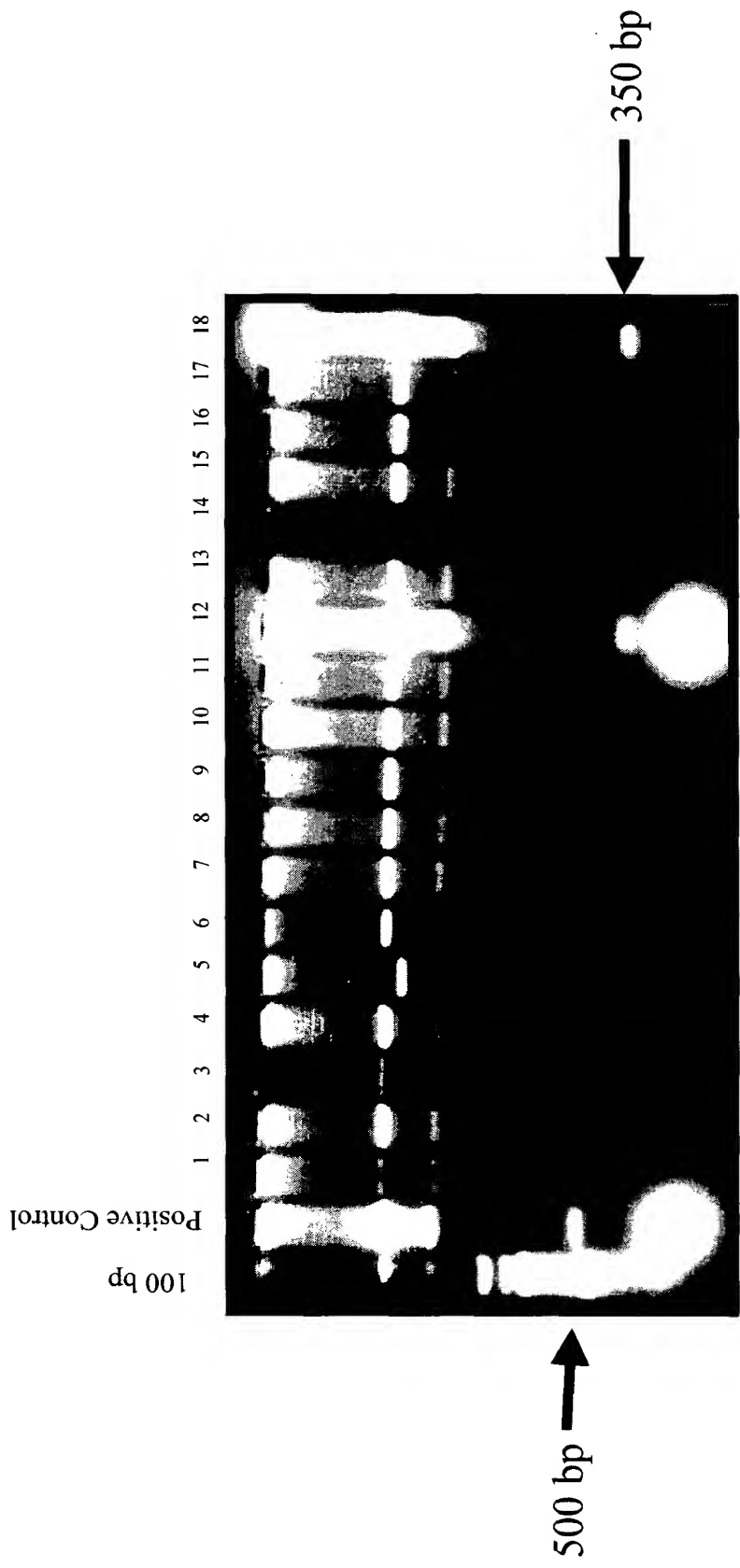


Fig. 5.2

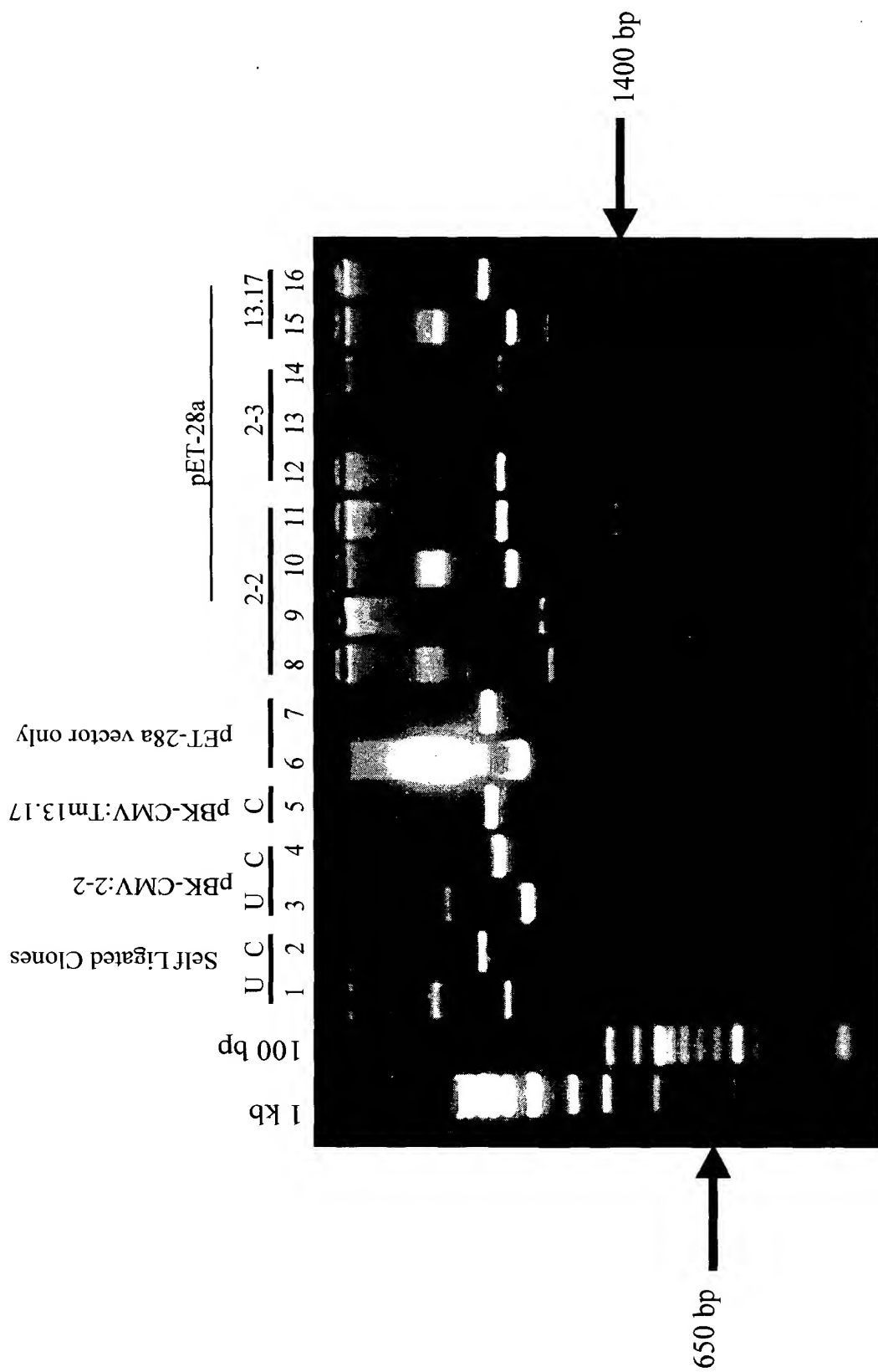


Fig. 5.3

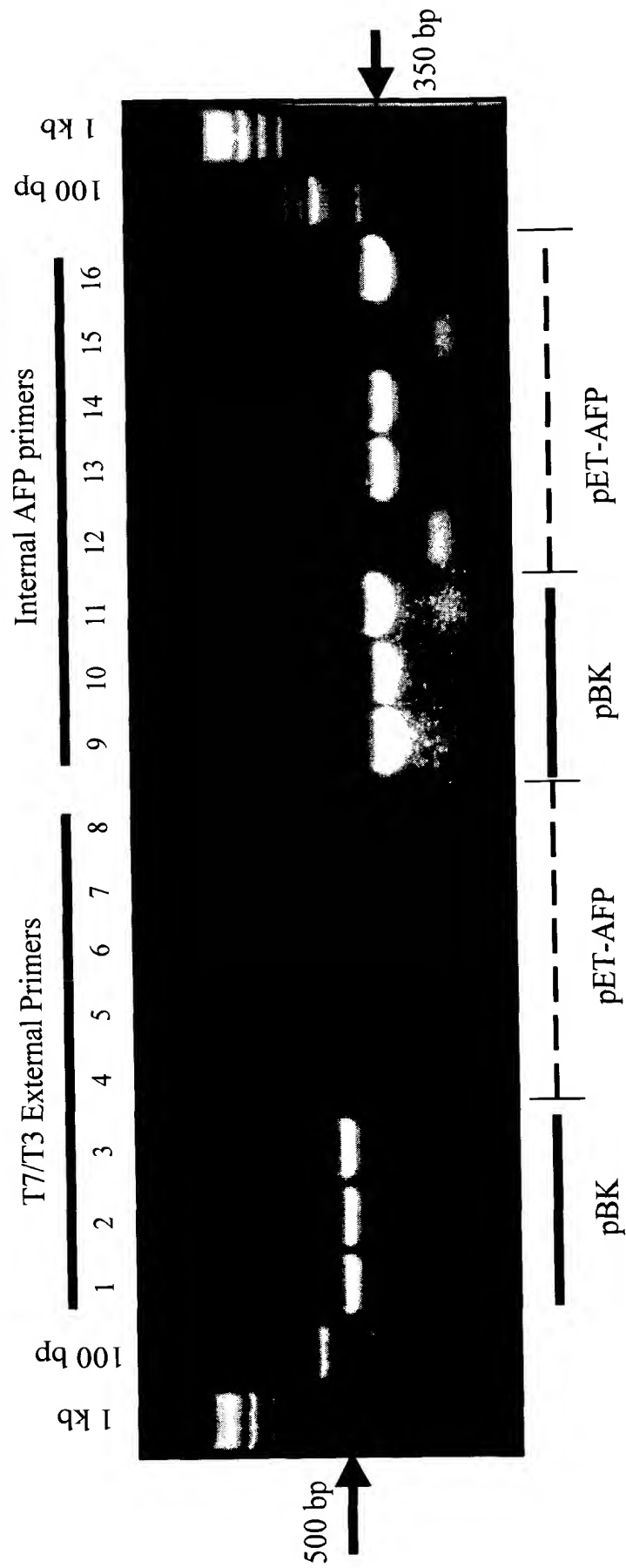


Fig. 5.4



Fig. 5.5

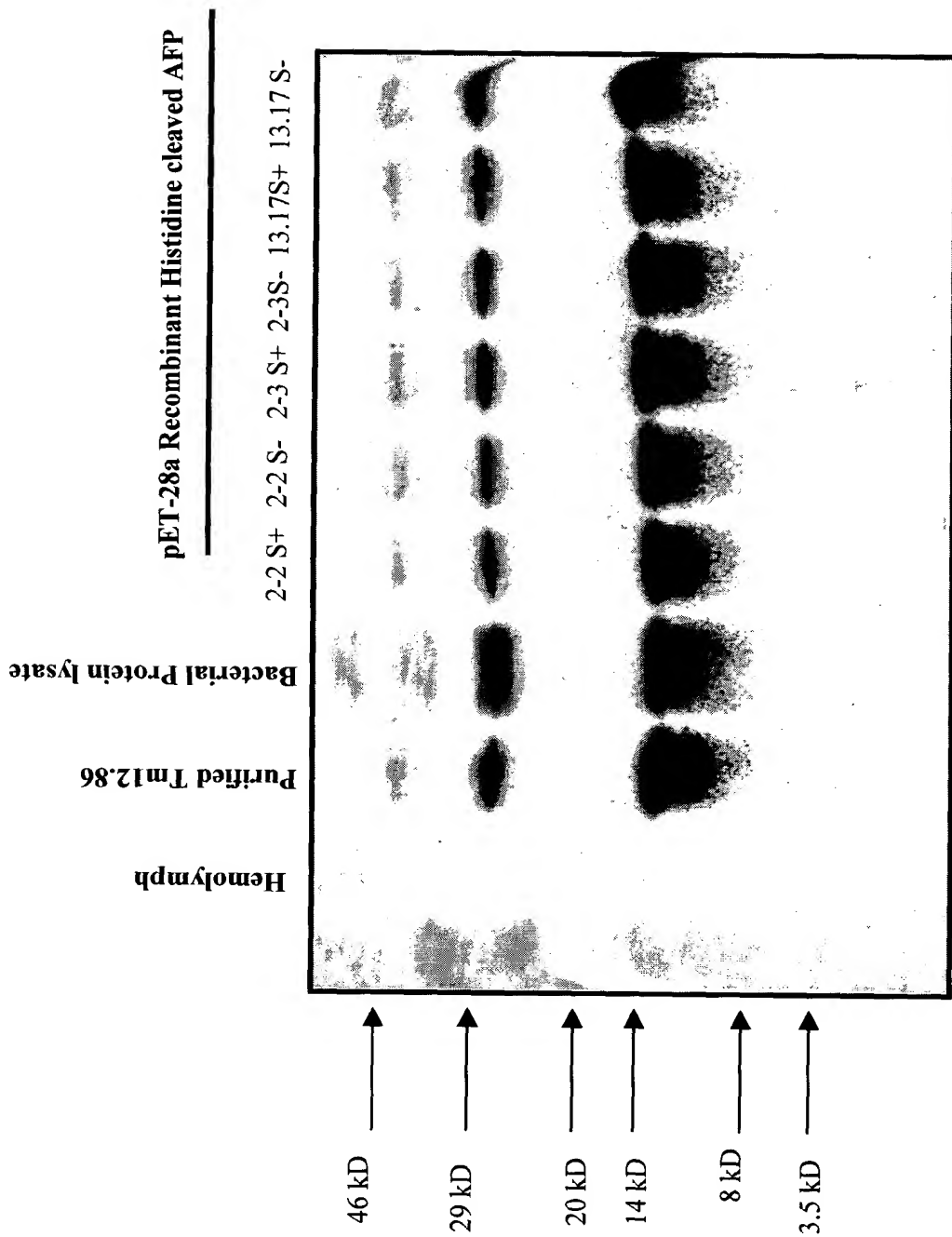


Fig 5.6

[illegible]

Fig. 5.7

His-tagged clone 2.2 without signal sequence

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
<div>His-tag Start Codon</div> <div>AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC</div> <div>Met Gly Ser Ser His His His His His His Ser</div> <div>-30 -25</div>	96
<div>AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT</div> <div>Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly</div> <div>-20 -15 -10</div>	141
<div>N-terminal of mature AFP</div> <div>GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG</div> <div>Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln</div> <div>-5 1 5</div>	186
<div>AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG</div> <div>Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val</div> <div>10 15 20</div>	231
<div>TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT</div> <div>Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp</div> <div>25 30 35</div>	276
<div>GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT</div> <div>Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr</div> <div>40 45 50</div>	321
<div>GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA</div> <div>Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys</div> <div>55 60 65</div>	366
<div>GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC</div> <div>Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile</div> <div>70 75 80</div>	411
<div>GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT</div> <div>Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala</div> <div>85 90 95</div>	456
<div>TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT</div> <div>Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser</div> <div>100 105 110</div>	501
<div>Stop Codon</div> <div>CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT</div> <div>Pro Ile Asp *</div> <div>115</div>	543

Fig. 5.8

His-tagged clone 2.3 with signal sequence

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG 50

His-tag Start Codon
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC 96
Met Gly Ser Ser His His His His His His Ser
-55 -50

AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT 141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly
-45 -40 -35

AFP Start Codon
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG 186
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met
-30 -25 -20

AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT 231
Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala
-15 -10 -5

N-terminal of Mature AFP
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC 276
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser
1 5 10

AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC 321
Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp
15 20 25

AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG 366
Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys
30 35 40

CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC 411
His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala
45 50 55

GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG 456
Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val
60 65 70

GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC 501
Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val
75 80 85

AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT 546
Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys
90 95 100

Stop Codon
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTGTGTA 595
Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *
105 110 115

Polyadenylation signal Poly-A tail
TTTGACTGAA TTTTGACAAT AAAGGTACTA TCGTTATGAA AAAAAAAAAA 645

AAAAAACTC GAGCACCACC ACCACCACCA CTGAGAT 682

Fig. 5.9

His-tagged Clone 2.3 without signal sequence

TTGTTAGCGG ATGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
His-tag Start Codon	
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-30 -25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-20 -15 -10	
N-terminal of mature AFP	
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG	186
Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln	
-5 1 5	
AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG	231
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val	
10 15 20	
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT	276
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp	
25 30 35	
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT	321
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr	
40 45 50	
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA	366
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys	
55 60 65	
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC	411
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile	
70 75 80	
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT	456
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala	
85 90 95	
TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT	501
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser	
100 105 110	
Stop Codon	
CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT	543
Pro Ile Asp *	
115	

Fig. 5.10

His-tagged Tm 13.17 with signal sequence

TTGTTAGCGG ATGGAATTC CTCGTAGGGG ATAATTTTGT TTACTTTAAG 50

His-tag Start Codon

AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC 96
Met Gly Ser Ser His His His His His Ser
-65 -60 -55

AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT 141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly
-50 -45 -40

GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC TGG ATC CAA AGA ATT 186
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Trp Ile Gln Arg Ile
-35 -30 -25

AFP Start Codon

CGG CAC GAG ACT ACT AAG ATG AAG TTG CTC TGT TGT CTA ATC TCC 231
Arg His Glu Thr Thr Lys Met Lys Leu Leu Cys Cys Leu Ile Ser
-20 -15 -10

N-terminal of mature AFP

CTC ATT CTG TTG GTC ACA GTT CAG GCC CTG ACC GAG GCA CAA ATT 276
Leu Ile Leu Leu Val Thr Val Gln Ala Leu Thr Glu Ala Gln Ile
-5 1 5

GAG AAA CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA 321
Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly
10 15 20

GTG TCG CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG 366
Val Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu
25 30 35

GAC GAT CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC 411
Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn
40 45 50

GCC GGT CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG 456
Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu
55 60 65

AGG GAG AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG 501
Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu
70 75 80

AAA ATC ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG 546
Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu
85 90 95

ACG GTG TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG 595
Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys
100 105 110

Stop Codon

TTC TCA CCA GTT GAT TGA ACCACCACGA CTAGTAGATG GTTCAAATGG 643
Phe Ser Pro Val Asp *
115

Polyadenylation signal Poly-A tail

TGTGCTTTAC ATATAAAAT AAAGTGTTC TGATGTAAAA AAAAAAAAAA 693

AAAAAAAAA AACTCGAGAG TATTCTAGAG CGGCCGCGGG CCCATCGTTT 743

TCCACCCCTC GAGCACCACC ACCACCACCA CTGAGAT 777

Fig. 5.11

SECRET

Fig. 5.12

09876349.012802

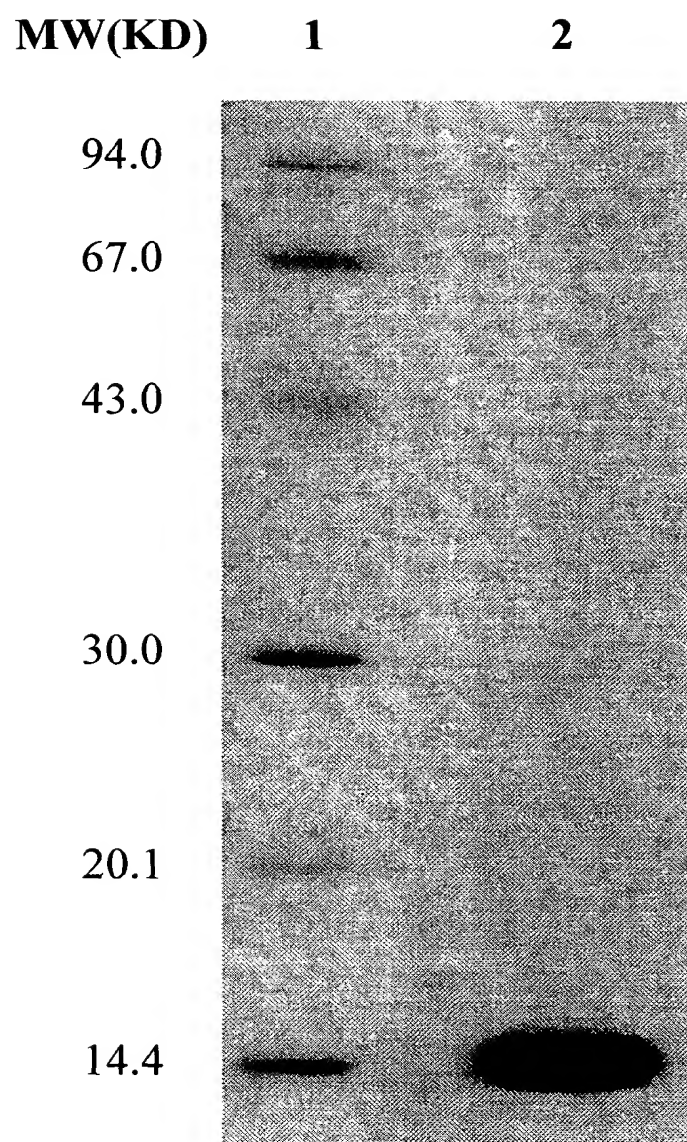


Fig. 6.0

09076349.012802

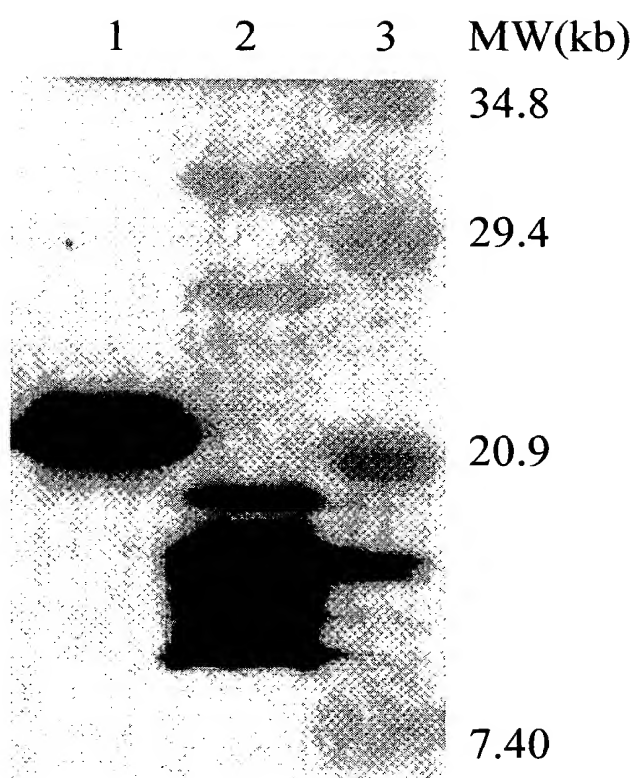


Fig. 6.1



Fig. 6.2

203270" 91592860

Tm 13.17 S-graph data

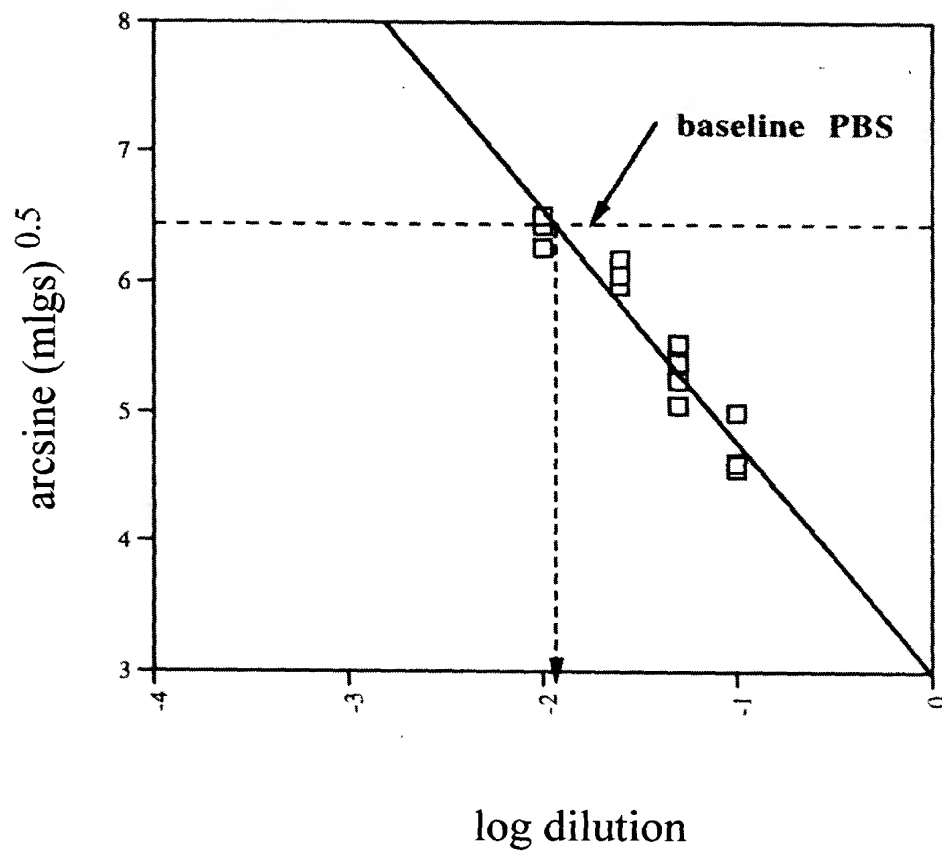


Fig. 6.3

ONE LETTER	NAME	THREE LETTER	CHEMICAL CLASS	HYDROPHOBICITY	Reactivity
A	Alanine	Ala	aliphatic	mod. hydrophobic	low
B	Asp or Asn	Asx			
C	Cysteine	Cys	sulfhydryl	hydrophobic	high
D	Aspartic Acid	Asp	acidic	highly hydrophilic	high
E	Glutamic Acid	Glu	acidic	highly hydrophilic	high
F	Phenylalanine	Phe	aromatic	highly hydrophobic	low
G	Glycine	Gly	aliphatic	mod. hydrophobic	low
H	Histidine	His	basic, imidazole	highly hydrophilic	high
I	Isoleucine	Ile	aliphatic	hydrophobic	low
J					
K	Lysine	Lys	basic	highly hydrophilic	high
L	Leucine	Leu	aliphatic	hydrophobic	low
M	Methionine	Met	sulfhydryl	hydrophobic	low
N	Asparagine	Asn	amide, acidic derived	hydrophilic	high
O					
P	Proline	Pro	aliphatic, cyclic, imino	mod. hydrophilic	low
Q	Glutamine	Gln	amide, acidic derived	hydrophilic	high
R	Arginine	Arg	basic	highly hydrophilic	high
S	Serine	Ser	aliphatic hydroxyl	hydrophilic	high
T	Threonine	Thr	aliphatic hydroxyl	hydrophilic	high
U					
V	Valine	Val	aliphatic	hydrophobic	low
W	Tryptophan	Trp	aromatic	highly hydrophobic	low
X					
Y	Tyrosine	Tyr	aromatic	mod. hydrophilic	high
Z	Glu or Gln	Glx			
		ACD	Any Acidic		
		ALP	Any Aliphatic		
		ALH	Any Aliphatic Hydroxyl		
		ARO	Any Aromatic		
		BAS	Any Basic		
		HY-	Hydrophobic		
		HY+	Hydrophilic		

Fig. 7.1

Position	Tm12.84-2.2	Tm12.84-2.3	Tm12.84-3.4	Tm12.84-3.9	Tm12.84-7.5	Consensus of Tm12.84	Tm13.17	Consensus with Tm13.17	B1	Consensus with B1	AFP-3	Consensus with AFP-3
1	A	A	A	A	A	A	A	A		A	C	A
2	C	C	C	C	C	C	G	N		N	A	N
3	G	G	G	G	G	G	A	R		R	G	R
4	A	A	A	A	A	A	C	N		N	T	N
5	G	G	G	G	G	G	T	N		N	C	N
6	C	C	C	C	C	C	A	N		N	C	N
7	A	A	A	A	A	A	A	A		N	C	N
8	A	A	A	A	A	A	T	A		N	G	N
9	A	A	A	A	A	A	A	A		N	A	N
10	A	A	A	A	A	A	G	R		N	A	N
11	A	A	A	A	A	A				N	A	N
12										N	A	N
13	A	A	A	A	A	A	A	A	A?	A	A	A
14	T	T	T	T	T	T	G	G	T?	G	G	G
15	G	G	G	G	G	G	A	A	G?	A	A	A
16	A	A	A	A	A	A	A	A		A	A	A
17	A	A	A	A	A	A	G	R		A	G	R
18	A	A	A	A	A	A	T	Y		A	C	Y
19	C	C	C	C	C	C	T	T		C/G	T	T
20	T	T	T	T	T	T	C	C		C	C	C
21	C	C	C	C	C	C	T	T		C	C	C
22	C	C	C	C	C	C	T	T		C	C	C
23	T	T	T	T	T	T	T	T		C	T	T
24	T	T	T	T	T	T	T	T		C	T	T
25	T	T	T	T	T	T	T	T		C	T	T
26	T	T	T	T	T	T	T	T		C	T	T
27	G	G	G	G	G	G	T	T		C	T	T
28	T	T	T	T	T	T	T	T		C	T	T
29	G	G	G	G	G	G	T	T		C	T	T
30	C	C	C	C	C	C	T	T		C	T	T
31	T	T	T	T	T	T	T	T		C	T	T
32	T	T	T	T	T	T	T	T		C	T	T
33	T	T	T	T	T	T	T	T		C	T	T
34	G	G	G	G	G	G	A	A		T/A	T	T/A
35	G	G	G	G	G	G	T	T		R	T	R
36	T	T	T	T	T	T	C	C		R	T	R
37	T	T	T	T	T	T	N	N		T	C	T
38	T	T	T	T	T	T	T	T		T	C	T
39	C	C	C	C	C	C	C	C		Y	C	Y
40	C	C	C	C	C	C	C	C		G/C	G	G/C
41	C	C	C	C	C	C	C	C		C	T	C
42	C	C	C	C	C	C	C	C		C	T	C
43	C	C	C	C	C	C	C	C		C	T	C
44	C	C	C	C	C	C	C	C		C	T	C
45	C	C	C	C	C	C	C	C		C	T	C
46	C	C	C	C	C	C	C	C		C	T	C
47	C	C	C	C	C	C	C	C		C	T	C
48	C	C	C	C	C	C	C	C		C	T	C
49	C	C	C	C	C	C	C	C		C	T	C
50	T	T	T	T	T	T	T	T		C/G	T	C/G
51	C	C	C	C	C	C	T	T		C/G	T	C/G
52	A	A	A	A	A	A	T	T		R	T	R
53	T	T	T	T	T	T	C	C		T	C	T
54	C	C	C	C	C	C	G	G		C	C	C
55	G	G	G	G	G	G	A	A		G/C	G	G/C
56	A	A	A	A	A	A	G	G		A	C	A
57	G	G	G	G	G	G	C	C		Y	T	Y
58	C	C	C	C	C	C	T	T		T	C	T
59	T	T	T	T	T	T	C	C		A	C	A
60	T	T	T	T	T	T	C	C		A	C	A
61	C	C	C	C	C	C	A	A		G	C	G
62	A	A	A	A	A	A	G	G		A	C	A
63	G	G	G	G	G	G	C	C		G	C	G
64	C	C	C	C	C	C	C	C		C	T	C
65	T	T	T	T	T	T	T	T		C	T	C
66	C	C	C	C	C	C	T	T		C	T	C
67	T	T	T	T	T	T	C	C		A	C	A
68	C	C	C	C	C	C	C	C		A	C	A
69	C	C	C	C	C	C	C	C		A	C	A
70	A	A	A	A	A	A	C	C		C	T	C
71	C	C	C	C	C	C	C	C		G/C	T	G/C
72	C	C	C	C	C	C	G	G		A	C	A
73	G	G	G	G	G	G	A	A		A	C	A
74	A	A	A	A	A	A	Y	Y		A	C	A
75	A	A	A	A	A	A	A	A		A	C	A
76	A	A	A	A	A	A	A	A		A	C	A
77	A	A	A	A	A	A	A	A		A	C	A
78	A	A	A	A	A	A	A	A		A	C	A
79	A	A	A	A	A	A	A	A		A	C	A
80	A	A	A	A	A	A	A	A		A	C	A
81	G	G	G	G	G	G	A	A		A	C	A
82	A	A	A	A	A	A	T	T		A	C	A
83	T	T	T	T	T	T	A	A		A	C	A
84	A	A	A	A	A	A	C	C		A	C	A
85	C	C	C	C	C	C	A	A		A	C	A
86	A	A	A	A	A	A	G	G		A	C	A
87	G	G	G	G	G	G	A	A		A	C	A
88	A	A	A	A	A	A	A	A		A	C	A
89	A	A	A	A	A	A	A	A		A	C	A
90	A	A	A	A	A	A	A	A		A	C	A
91	A	A	A	A	A	A	A	A		A	C	A
92	G	G	G	G	G	G	T	T		A	C	A
93	A	A	A	A	A	A	G	G		A	C	A
94	A	A	A	A	A	A	A	A		A	C	A
95	C	C	C	C	C	C	A	A		A	C	A
96	A	A	A	A	A	A	A	A		A	C	A
97	A	A	A	A	A	A	A	A		A	C	A
98	A	A	A	A	A	A	A	A		A	C	A
99	G	G	G	G	G	G	A	A		A	C	A
100	A	A	A	A	A	A	T	T		A	C	A
101	T	T	T	T	T	T	C	C		A	C	A
102	C	C	C	C	C	C	A	A		A	C	A
103	A	A	A	A	A	A	C	C		A	C	A
104	G	G	G	G	G	G	A	A		A	C	A
105	C	C	C	C	C	C	A	A		A	C	A
106	A	A	A	A	A	A	A	A		A	C	A
107	A	A	A	A	A	A	A	A		A	C	A
108	A	A	A	A	A	A	A	A		A	C	A
109	G	G	G	G	G	G	A	A		A	C	A
110	A	A	A	A	A	A	T	T		A	C	A
111	T	T	T	T	T	T	G	G		A	C	A
112	G	G	G	G	G	G	C	C		A	C	A
113	C	C	C	C	C	C	A	A		A	C	A
114	C	C	C	C	C	C	A	A		A	C	A
115	A	A	A	A	A	A	A	A		A	C	A
116	G	G	G	G	G	G	A	A		A	C	A
117	A	A	A	A	A	A	A	A		A	C	A

Fig. 7.2

Position	Tm12.84-2.2	Tm12.84-2.3	Tm12.84-3.4	Tm12.84-3.9	Tm12.84-7.5	Consensus of	Tm13.17	Consensus with	B1	Consensus with	AFP-3	Consensus with
118	C	C	C	C	C	C	A	N	A	N	C	N
119	A	A	A	A	A	A	T	A	C	N	T	N
120	G	G	G	G	G	G	G	A	T	N	G	N
121	T	T	T	T	T	T/A	A	A	A	G	A	A/T
122	G	G	G	G	G	G	A	A	A	T/A	T	T/A
123	T	T	T	T	T	T	G	C/G	G	C/G	C	C/G
124	C	C	C	C	C	C	T	Y	T	Y	T	Y
125	C	C	C	C	C	C	G	G	G	G	G	G
126	G	G	G	G	G	G	A	A	A	A	A	A
127	G	G	G	G	G	G	G	G	G	G	G	G
128	A	A	A	A	A	A	G	G	A	A	A	A
129	G	G	G	G	G	G	T	T	T	T	T	T
130	T	T	T	T	T	T	T	T	T	T	T	T
131	G	G	G	G	G	G	T	T	T	T	T	T
132	T	T	T	T	T	T	C	C	C	C	C	C
133	C	C	C	C	C	C	G	C/G	C	C/G	T	N
134	C	C	C	C	C	C	C	C	G	C/G	G	C/G
135	C	C	C	C	C	C	A	A	A	A	A	A
136	A	A	A	A	A	A	A	A	A	A	A	A
137	A	A	A	A	A	A	G	A	A	A	A	A
138	G	G	G	G	G	G	A	A	A	A	A	A
139	A	A	A	A	A	A	G	A	A	A	A	A
140	A	A	A	A	A	A	A	A	C	G/C	G	G/C
141	G	G	G	G	G	G	A	Y	T	R	T	N
142	C	C	C	C	C	C	C	G/C	C	G/C	C	G/C
143	G	G	G	G	G	G	A	A	A	A	A	A
144	A	A	A	A	A	A	T	A	A	A	A	A
145	T	T	T	T	T	T	A	A	A	A	A	A
146	C	C	C	C	C	C	A	A	A	A	A	A
147	G	G	G	G	G	G	A	A	A	A	A	A
148	A	A	A	A	A	A	C	A	A	A	A	A
149	C	C	C	C	C	C	C	A	A	A	A	A
150	A	A	A	A	A	A	A	A	A	A	A	A
151	A	A	A	A	A	A	A	A	A	A	A	A
152	A	A	A	A	A	A	A	A	A	A	A	A
153	G	G	G	G	G	G	G	A	A	A	A	A
154	T	T	T	T	T	T	T	C	A	A	A	A
155	C	C	C	C	C	C	T	Y	T	T	T	T
156	C	C	C	C	C	C	C	C	C	C	C	C
157	G	G	G	G	G	G	C	G	C	C	C	C
158	C	C	C	C	C	C	A	A	A	A	A	A
159	A	A	A	A	A	A	A	A	A	A	A	A
160	A	A	A	A	A	A	A	A	A	A	A	A
161	A	A	A	A	A	A	C	A	A	A	A	A
162	A	A	A	A	A	A	C	A	A	A	A	A
163	G	G	G	G	G	G	G	G	A	A	A	A
164	T	T	T	T	T	T	T	T	G	A	A	A
165	G	G	G	G	G	G	G	T	T	T	T	T
166	T	T	T	T	T	T	A	T/A	T	T/A	T	T/A
167	C	C	C	C	C	C	C	C	A	A	A	A
168	T	T	T	T	T	T	T	N	T	N	T	N
169	T	T	T	T	T	T	G	G	T	G	T	G
170	T	T	T	T	T	T	G	G	T	T	T	T
171	G	G	G	G	G	G	G	G	T	T	T	T
172	T	T	T	T	T	T	A	T/A	A	T/A	T	T/A
173	C	C	C	C	C	C	G	C/G	G	C/G	G	C/G
174	G	G	G	G	G	G	A	A	A	A	A	A
175	A	A	A	A	A	A	C	A	A	A	A	A
176	T	T	T	T	T	T	G	A	A	A	A	A
177	G	G	G	G	G	G	G	G	C	G	C	G
178	A	A	A	A	A	A	A	A	A	A	A	A
179	T	T	T	T	T	T	C	T	C	C	C	C
180	C	C	C	C	C	C	C	C	C	C	C	C
181	C	C	C	C	C	C	C	C	C	C	C	C
182	C	C	C	C	C	C	A	A	A	A	A	A
183	A	A	A	A	A	A	A	A	A	A	A	A
184	A	A	A	A	A	A	A	A	A	A	A	A
185	A	A	A	A	A	A	A	A	A	A	A	A
186	A	A	A	A	A	A	A	A	A	A	A	A
187	A	A	A	A	A	A	T	N	C	N	C	N
188	G	G	G	G	G	G	G	A	A	A	A	A
189	A	A	A	A	A	A	A	A	A	A	A	A
190	A	A	A	A	A	A	A	A	A	A	A	A
191	G	G	G	G	G	G	A	R	A	R	A	R
192	A	A	A	A	A	A	C	N	A	N	A	N
193	A	A	A	A	A	A	C	R	A	R	A	R
194	G	G	G	G	G	G	C	G/C	G	G/C	G	G/C
195	C	C	C	C	C	C	A	A	A	A	A	A
196	A	A	A	A	A	A	A	A	A	A	A	A
197	C	C	C	C	C	C	G	A	A	A	A	A
198	G	G	G	G	G	G	T	N	C	N	C	N
199	T	T	T	T	T	T	T	G	T	G	T	G
200	T	T	T	T	T	T	T	Y	T	Y	T	Y
201	C	C	C	C	C	C	T	Y	T	Y	T	Y
202	T	T	T	T	T	T	T	Y	T	Y	T	Y
203	C	C	C	C	C	C	T	T	T	T	T	T
204	T	T	T	T	T	T	T	T	T	T	T	T
205	G	G	G	G	G	G	G	C	A	C	A	C
206	C	C	C	C	C	C	T	N	T	N	T	N
207	T	T	T	T	T	T	T	C	T	C	T	C
208	T	T	T	T	T	T	T	C	T	C	T	C
209	C	C	C	C	C	C	T	C	T	C	T	C
210	T	T	T	T	T	T	C	C	T	C	T	C
211	C	C	C	C	C	C	G	G/C	C	G/C	G	G/C
212	G	G	G	G	G	G	A	A	A	A	A	A
213	A	A	A	A	A	A	A	R	A	R	A	R
214	A	A	A	A	A	A	A	G	A	G	A	G
215	G	G	G	G	G	G	A	A	A	A	A	A
216	A	A	A	A	A	A	A	R	A	R	A	R
217	A	A	A	A	A	A	A	N	A	N	A	N
218	A	A	A	A	A	A	C	C	A	C	A	C
219	A	A	A	A	A	A	C	C	A	C	A	C
220	C	C	C	C	C	C	G	G	A	A	A	A
221	T	T	T	T	T	T	T	G	A	A	A	A
222	G	G	G	G	G	G	G	A	A	A	A	A
223	A	A	A	A	A	A	T	G	A	A	A	A
224	G	G	G	G	G	G	T	G	A	A	A	A
225	A	A	A	A	A	A	C	A	A	A	A	A
226	G	G	G	G	G	G	T	G/C	T	T	T	T
227	T	T	T	T	T	T	G	A	A	A	A	A
228	G	G	G	G	G	G	G	C	A	A	A	A
229	C	C	C	C	C	C	C	C	C	C	C	C
230	A	A	A	A	A	A	C	N	C	C	C	C
231	A	A	A	A	A	A	C	C	C	C	C	C
232	C	C	C	C	C	C	G	C/G	G	C/G	G	C/G
233	C	C	C	C	C	C	G					
234	C	C	C	C	C	C	G					
235	G	G	G	G	G	G	G					

Fig. 7.2 cont.

Position	Tm12.84-2.2	Tm12.84-2.3	Tm12.84-3.4	Tm12.84-3.9	Tm12.84-7.5	Consensus of	Tm13.17	Consensus with	B1	Consensus with	AFP-3	Consensus with
236	A	A	A	A	A	A	A	A	A	A	C	N
237	A	A	A	A	A	A	A	A	A	A	C	N
238	G	G	G	G	G	G	T	C	C	C	A	C/G
239	C	C	C	C	C	C	C	G	G	G	G	N
240	C	C	C	C	C	C	G	G	G	G	G	G
241	G	G	G	G	G	G	A	G	A	A	G	A/T
242	G	G	G	G	G	G	A	G	A	A	A	N
243	A	A	A	A	A	A	A	G	A	A	A	N
244	A	A	A	A	A	A	A	G	A	A	A	N
245	C	C	C	C	C	C	A	C	A	A	A	N
246	A	A	A	A	A	A	G	R	R	R	T	N
247	C	C	C	C	C	C	T	G	T	T	T	N
248	C	C	C	C	C	C	G	C	C	C	C	N
249	C	C	C	C	C	C	T	G	T	T	C	N
250	A	A	A	A	A	A	G	R	R	R	C	N
251	A	A	A	A	A	A	T	N	A	A	A	A/T
252	T	T	T	T	T	T	G	G	G	G	A	G/C
253	G	G	G	G	G	G	T	C	C	C	G	Y
254	T	T	T	T	T	T	C	G	G	G	G	G/C
255	G	G	G	G	G	G	A	G	A	A	A	A
256	A	A	A	A	A	A	C	C	C	C	C	G/C
257	G	G	G	G	G	G	G	G	G	G	C	N
258	A	A	A	A	A	A	T	R	R	R	A	N
259	G	G	G	G	G	G	T	R	R	R	A	N
260	T	T	T	T	T	T	G	Y	Y	Y	C	N
261	A	A	A	A	A	A	T	T	T	T	T	N
262	C	C	C	C	C	C	G	C	C	C	A	N
263	T	T	T	T	T	T	T	T	T	T	T	T
264	C	C	C	C	C	C	G	C	C	C	T	N
265	A	A	A	A	A	A	A	R	R	R	A	A
266	A	A	A	A	A	A	G	R	R	R	G	R
267	G	G	G	G	G	G	C	G	G	G	A	R
268	C	C	C	C	C	C	A	N	A	A	C	N
269	C	C	C	C	C	C	G	C	C	C	G	C/G
270	A	A	A	A	A	A	A	A	A	A	A	A
271	A	A	A	A	A	A	A	A	A	A	A	A
272	G	G	G	G	G	G	G	G	G	G	A	R
273	C	C	C	C	C	C	G	C	C	C	T	N
274	T	T	T	T	T	T	T	T	T	T	T	T
275	G	G	G	G	G	G	G	G	G	G	C	G/C
276	A	A	A	A	A	A	A	R	R	R	A	N
277	A	A	A	A	A	A	G	R	R	R	A	N
278	G	G	G	G	G	G	A	G	A	A	G	N
279	C	C	C	C	C	C	A	N	A	A	A	N
280	A	A	A	A	A	A	G	N	A	A	A	N
281	T	T	T	T	T	T	T	T	T	T	A	R
282	C	C	C	C	C	C	G	C	C	C	A	N
283	G	G	G	G	G	G	T	T	T	T	A	N
284	T	T	T	T	T	T	C	C	C	C	C	N
285	G	G	G	G	G	G	A	C	A	A	T	N
286	G	G	G	G	G	G	C	R	C	C	C	N
287	C	C	C	C	C	C	T	Y	A	A	T	N
288	A	A	A	A	A	A	G	R	R	R	G	N
289	G	G	G	G	G	G	C	C	C	C	A	N
290	C	C	C	C	C	C	A	A	A	A	G	C/G
291							A	A	A	A	G	R
292							C	C	C	C	A	A/T
293							A	A	A	A	T	N
294							G	G	G	G	T	N
295	G	G	G	G	G	G	A	A	A	A	C	C/G
296	A	A	A	A	A	A	G	A	A	A	G	R
297	C	C	C	C	C	C	A	C	C	C	A	R
298	G	G	G	G	G	G	A	G	A	A	A	A
299	A	A	A	A	A	A	A	R	R	R	A	R
300	A	A	A	A	A	A	A	C	C	C	G	Y
301	G	G	G	G	G	G	T	N	N	N	T	N
302	A	A	A	A	A	A	G	G	A	A	C	R
303	G	G	G	G	G	G	A	A	A	A	A	R
304	T	T	T	T	T	T	G	A	G	G	T	R
305	G	G	G	G	G	G	A	C	C	C	N	R
306	A	A	A	A	A	A	G	A	A	A	A	R
307	C	C	C	C	C	C	A	C	C	C	T	N
308	A	A	A	A	A	A	A	C	A	A	A	R
309	A	A	A	A	A	A	A	A	A	A	G	R
310	A	A	A	A	A	A	A	A	A	A	A	R
311	G	G	G	G	G	G	A	R	R	R	C	N
312	A	A	A	A	A	A	T	A	T	T	T	A/T
313	T	T	T	T	T	T	C	R	C	C	G	C/G
314	C	C	C	C	C	C	A	T	T	T	T	N
315	T	T	T	T	T	T	T	T	T	T	T	Y
316	G	G	G	G	G	G	C	G	G	G	T	N
317	C	C	C	C	C	C	A	A	A	A	G	N
318	A	A	A	A	A	A	G	A	A	A	A	N
319	G	G	G	G	G	G	A	A	A	A	C	N
320	A	A	A	A	A	A	T	A	A	A	C	N
321	G	G	G	G	G	G	A	A	A	A	A	N
322	A	A	A	A	A	A	G	A	A	A	A	N
323	A	A	A	A	A	A	T	G	T	T	A	N
324	G	G	G	G	G	G	G	G	G	G	T	N
325	T	T	T	T	T	T	C	C	C	C	G	N
326	G	G	G	G	G	G	G	Y	G	G	C	G/C
327	T	T	T	T	T	T	C	C	C	C	T	N
328	G	G	G	G	G	G	G	G	G	G	C	G/C
329	T	T	T	T	T	T	T	T	T	T	C	N
330	G	G	G	G	G	G	G	G	G	G	C	G/C
331	T	T	T	T	T	T	C	T	T	T	G	N
332	C	C	C	C	C	C	A	A	A	A	T	N
333	A	A	A	A	A	A	A	A	A	A	A	N
334	A	A	A	A	A	A	G	A	A	A	A	N
335	G	G	G	G	G	G	A	A	A	A	A	N
336	A	A	A	A	A	A	G	A	A	A	A	N
337	A	A	A	A	A	A	A	R	R	R	A	A
338	G	G	G	G	G	G	G	R	R	R	A	N
339	C	C	C	C	C	C	A	N	A	A	A	N
340	C	C	C	C	C	C	T	Y	C	C	A	N
341	C	C	C	C	C	C	C	A	A	A	C	N
342	A	A	A	A	A	A	T	C	C	C	T	N
343	C	C	C	C	C	C	T	T	T	T	C	N
344	A	A	A	A	A	A	G	A	A	A	A	N
345	C	C	C	C	C	C	A	A	A	A	A	N
346	C	C	C	C	C	C	T	T	T	T	C	N
347	A	A	A	A	A	A	G	Y	G	G	C	N
348	G	G	G	G	G	G	A	A	A	A	T	N
349	A	A	A	A	A	A	A	R	R	R	A	N
350	G	G	G	G	G	G	A	R	R	R	A	N
351	A	A	A	A	A	A	A	A	A	A	A	N
352	G	G	G	G	G	G	A	A	A	A	A	N
353	A	A	A	A	A	A	A	A	A	A	A	A/T

Fig. 7.2 cont.

Position	Tm12.84-2.2	Tm12.84-2.3	Tm12.84-3.4	Tm12.84-3.9	Tm12.84-7.5	Consensus of	Tm13.17	Consensus with	B1	Consensus with	AFP-3	Consensus with
354	A	A	A	A	A	A	G	R	A	R	C	N
355	A	A	A	A	A	A	A	A	C	N	T	N
356	C	C	C	C	C	C	C	C	G	C/G	C	C/G
357	G	G	G	G	G	G	G	G	C	G/C	C	G/C
358	G	G	G	G	G	G	G	G	A	N	T	N
359	C	C	C	C	C	C	T	Y	T	N	C	N
360	T	T	T	T	T	T	T	N	T	N	A	N
361	A	A	A	A	A	A	A	AT	AT	N	G	N
362	T	T	T	T	T	T	T	A	G	C	C	N
363	A	A	A	A	A	A	A	R	A	C	A	N
364	G	G	G	G	G	G	A	A	A	R	G	R
365	A	A	A	A	A	A	T	A	G	A	C	A
366	A	A	A	A	A	A	C	A	T	N	A	N
367	C	C	C	C	C	C	T	Y	AT	AT	C	AT
368	C	C	C	C	C	C	T	A	T	Y	T	Y
369	T	T	T	T	T	T	T	C	A	N	T	Y
370	T	T	T	T	T	T	T	T	A	Y	T	Y
371	T	T	T	T	T	T	T	T	C	N	T	Y
372	C	C	C	C	C	C	A	A	A	A	T	A
373	A	A	A	A	A	A	A	A	A	A	A	A
374	A	A	A	A	A	A	A	A	A	N	A	A
375	G	G	G	G	G	G	T	R	T	N	G	N
376	T	T	T	T	T	T	G	N	G	N	T	N
377	G	G	G	G	G	G	T	N	T	N	C	N
378	T	T	T	T	T	T	C	R	A	N	G	N
379	A	A	A	A	A	A	T	Y	T	T/A	T	T/A
380	T	T	T	T	T	T	C	AT	T	Y	C	Y
381	T	T	T	T	T	T	A	C/G	A	AT	T	N
382	T	T	T	T	T	T	T	R	G	N	A	N
383	A	A	A	A	A	A	G	A	A	R	C	R
384	C	C	C	C	C	C	A	A	G	R	G	R
385	G	G	G	G	G	G	A	A	A	N	A	N
386	C	C	C	C	C	C	A	A	C	N	A	N
387	A	A	A	A	A	A	A	R	A	A	C	A
388	A	A	A	A	A	A	A	Y	C	R	A	N
389	G	G	G	G	G	G	A	A	A	N	A	N
390	C	C	C	C	C	C	A	A	G	R	G	R
391	A	A	A	A	A	A	A	C	C	N	C	N
392	A	A	A	A	A	A	C	C	A	T/A	T	C
393	C	C	C	C	C	C	A	T/A	A	T/A	C	N
394	T	T	T	T	T	T	A	A	A	A	G	A
395	G	G	G	G	G	G	A	R	C	R	C	Y
396	T	T	T	T	T	T	C	C	C	C	T	C
397	G	G	G	G	G	G	A	T/A	A	T/A	G	N
398	A	A	A	A	A	A	A	A	A	R	A	A
399	A	A	A	A	A	A	A	A	A	AT	T	T
400	T	T	T	T	T	T	T	N	T	N	T	N
401	T	T	T	T	T	T	T	T	T	Y	Y	Y
402	T	T	T	T	T	T	T	T	T	Y	Y	Y
403	C	C	C	C	C	C	C	C	C	N	C	N
404	T	T	T	T	T	T	C	T/A	G	N	T	N
405	C	C	C	C	C	C	A	C	A	N	C	N
406	T	T	T	T	T	T	A	A	A	R	Y	R
407	A	A	A	A	A	A	T	T	A	Y	T	T
408	T	T	T	T	T	T	G	A	T	AT	T	T
409	A	A	A	A	A	A	A	T	T	T	A	A
410	T	T	T	T	T	T	A	T	T	T	T	T
411	T	T	T	T	T	T	A	T	T	T	T	T
412	G	G	G	G	G	G	A	T	T	T	T	T
413	A	A	A	A	A	A	A	T	T	T	T	T
414	T	T	T	T	T	T	A	T	T	T	T	T
415	T	T	T	T	T	T	A	T	T	T	T	T
416	T	T	T	T	T	T	A	T	T	T	T	T
417	A	A	A	A	A	A	A	T	T	T	T	T
418	A	A	A	A	A	A	A	T	T	T	T	T
419	T	T	T	T	T	T	A	T	T	T	T	T
420	T	T	T	T	T	T	C	C	C	Y	G	N
421	T	T	T	T	T	T	C	A	A	G/C	G	N
422	T	T	T	T	T	T	C	A	A	T/A	G	N
423	T	T	T	T	T	T	C	A	A	N	T	N
424	T	T	T	T	T	T	C	A	A	N	T	N
425	T	T	T	T	T	T	C	A	A	N	T	N
426	T	T	T	T	T	T	C	A	A	N	T	N
427	G	G	G	G	G	G	A	C	G	G/C	C	N
428	T	T	T	T	T	T	A	A	T	N	T	N
429	A	A	A	A	A	A	T	Y	Y	AT	C	N
430	T	T	T	T	T	T	T	T	T	N	T	N
431	T	T	T	T	T	T	T	T/A	T	T/A	G	T/A
432	T	T	T	T	T	T	G	N	G	N	A	N
433	G	G	G	G	G	G	T	N	N	N	A	N
434	A	A	A	A	A	A	A	N	N	N	A	N
435	C	C	C	C	C	C	A	R	R	R	T	AT
436	T	T	T	T	T	T	G	AT	A	AT	T	AT
437	A	A	A	A	A	A	T	N	A	N	A	N
438	A	A	A	A	A	A	G	T	T	T	T	N
439	T	T	T	T	T	T	T	T	T	T	T	T
440	T	T	T	T	T	T	C	Y	Y	Y	T	Y
441	T	T	T	T	T	T	A	A	A	A	T	A
442	T	T	T	T	T	T	A	A	A	A	T	A
443	T	T	T	T	T	T	A	A	A	A	T	A
444	G	G	G	G	G	G	A	A	A	A	T	A
445	A	A	A	A	A	A	T	G	T	G	T	A
446	C	C	C	C	C	C	T	T	T	T	T	A
447	A	A	A	A	A	A	G	G	G	G	T	N
448	A	A	A	A	A	A	T	T	T	T	T	N
449	A	A	A	A	A	A	G	T	T	T	T	R
450	A	A	A	A	A	A	T	T	T	T	T	T/A
451	A	A	A	A	A	A	T	T	T	T	T	R
452	A	A	A	A	A	A	T	T	T	T	T	Y
453	A	A	A	A	A	A	T	T	T	T	T	G/C
454	A	A	A	A	A	A	T	T	T	T	T	Y
455	A	A	A	A	A	A	T	T	T	T	T	N
456	A	A	A	A	A	A	T	T	T	T	T	Y
457	A	A	A	A	A	A	T	T	T	T	T	N
458	A	A	A	A	A	A	T	T	T	T	T	N
459	A	A	A	A	A	A	T	T	T	T	T	N
460	A	A	A	A	A	A	T	T	T	T	T	A
461	A	A	A	A	A	A	T	T	T	T	T	AT
462	A	A	A	A	A	A	T	T	T	T	T	T
463	A	A	A	A	A	A	T	T	T	T	T	AT
464	A	A	A	A	A	A	T	T	T	T	T	AT
465	A	A	A	A	A	A	T	T	T	T	T	AT
466	A	A	A	A	A	A	T	T	T	T	T	AT
467	A	A	A	A	A	A	T	T	T	T	T	N
468	A	A	A	A	A	A	T	T	T	T	T	N
469	A	A	A	A	A	A	T	T	T	T	T	R
470	A	A	A	A	A	A	T	T	T	T	T	T/A
471	A	A	A	A	A	A	T	T	T	T	T	G/C

Fig. 7.2 cont.

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Position	Tm12.84-2.2	Tm12.84-2.3	Tm12.84-3.4	Tm12.84-3.9	Tm12.84-7.5	Consensus of	Tm13.17	Consensus with	B1	Consensus with	AFP-3	Consensus with
472	A	A	A	A	A	A	A	A		A	A	A
473	A	A	A	A	A	A	A	A		A	A	A
474	T	T	T	T	T	T	T	T		T	T	T
475	A	A	A	A	A	A	A	A		A	A	A
476	A	A	A	A	A	A	A	A		A	A	A
477	A	A	A	A	A	A	A	A		A	A	A
478	G	G	G	G	G	G	G	G		G	G	G
479	G	G	G	G	G	G	G	G		G	G	G
480	T	T	T	T	T	T	T	T		T	T	T
481	A	A	A	A	A	A	A	A		A	A	A
482	A	C	C	C	C	C	T	T		Y	A	N
483	T	T	T	T	T	T	T	T		T	A	N
484	A	A	A	A	A	A	C	T		N	G	AT
485	T	T	T	T	T	T	T	T		T	A	N
486	C	C	C	C	C	C	G	T		N	A	AT
487	G	G	G	G	G	G	A	R		R	A	N
488	T	T	T	T	T	T	T	T		T	A	TIA
489	T	T	T	T	T	T	G	T		N	A	N
490	A	A	A	A	A	A	T	N		N	A	N
491	T	T	T	T	T	T	A	N		N	A	R
492	G	G	G	G	G	G	A	R		N	A	N
493	T	A	T	A	T	N	A	N		N	A	N
494	A	A	A	A	A	A	A	A		A	A	A
495	A	A	A	A	A	A	A	A		A	A	A
496	A	A	A	A	A	A	A	A		A	A	A
497	A	A	A	A	A	A	A	A		A	A	A
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499	A	A	A	A	A	A	A	A		A	A	A
500	A	A	A	A	A	A	A	A		A	A	A
501	A	A	A	A	A	A	A	A		A	A	A
502	A	A	A	A	A	A	A	A		A	A	A
503	A	A	A	A	A	A	A	A		A	A	A
504	A	A	A	A	A	A	A	A		A	A	A
505	A	A	A	A	A	A	A	A		A	A	A
506	A	A	A	A	A	A	A	A		A	A	A
507	A	A	A	A	A	A	A	A		A	A	A
508	A	A	A	A	A	A	A	A		A	A	A
509	A	A	A	A	A	A	A	A		A	A	A
510	A	A	A	A	A	A	A	A		A	A	A
511	A	A	A	A	A	A	A	A		A	A	A
512												

Fig. 7.2 cont.

Position	Tm 12.84-2.2	Tm 12.84-2.3	Tm 12.84-3.4	Tm 12.84-3.9	Tm 12.84-7.5	Consensus Tm 12.84	Tm 13.17	Consensus Tm 13.17	Tm P-81	Tm P-82	Consensus Tm P-82	Tm AFP-3	Consensus Tm AFP-3	GENERAL CONSENSUS	SUBSTITUTIONS - most to least common
1	M	M	M	M	M	M	M	M	M	M	M	M	M	M	
2	K	K	K	K	K	K	K	K	K	K	K	K	K	K	
3	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
4	L	L	L	L	L	L	L	L	L	L	L	L	L	L	
5	C	C	C	C	C	C	C	C	C	C	C	C	C	C	
6	F	F	F	F	F	F	F	F	F	F	F	F	F	F	
7	A	A	A	A	A	A	A	A	A	A	A	A	A	A	
8	A	A	A	A	A	A	A	A	A	A	A	A	A	A	
9	A	A	A	A	A	A	A	A	A	A	A	A	A	A	
10	A	A	A	A	A	A	A	A	A	A	A	A	A	A	
11	V	V	V	V	V	V	V	V	V	V	V	V	V	V	
12	V	V	V	V	V	V	V	V	V	V	V	V	V	V	
13	I	I	I	I	I	I	I	I	I	I	I	I	I	I	
14	A	A	A	A	A	A	A	A	A	A	A	A	A	A	
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17	V	V	V	V	V	V	V	V	V	V	V	V	V	V	
18	V	V	V	V	V	V	V	V	V	V	V	V	V	V	
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21	D	D	D	D	D	D	D	D	D	D	D	D	D	D	
22	E	E	E	E	E	E	E	E	E	E	E	E	E	E	
23	E	E	E	E	E	E	E	E	E	E	E	E	E	E	
24	I	I	I	I	I	I	I	I	I	I	I	I	I	I	
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76	K	K	K	K	K	K	K	K	K	K	K	K	K	K	
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Fig. 7.3

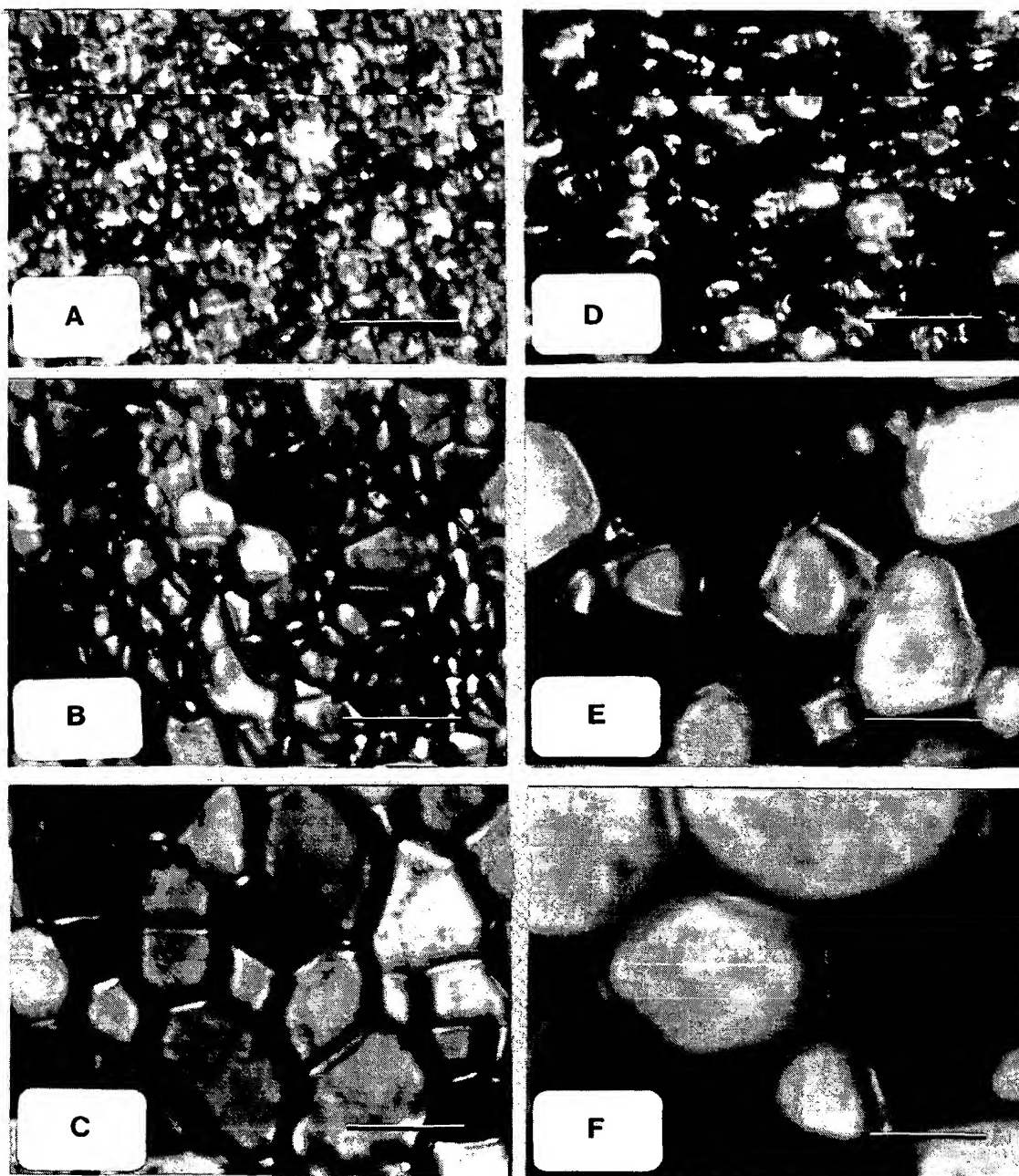


Fig. 8.0

09875349.012802

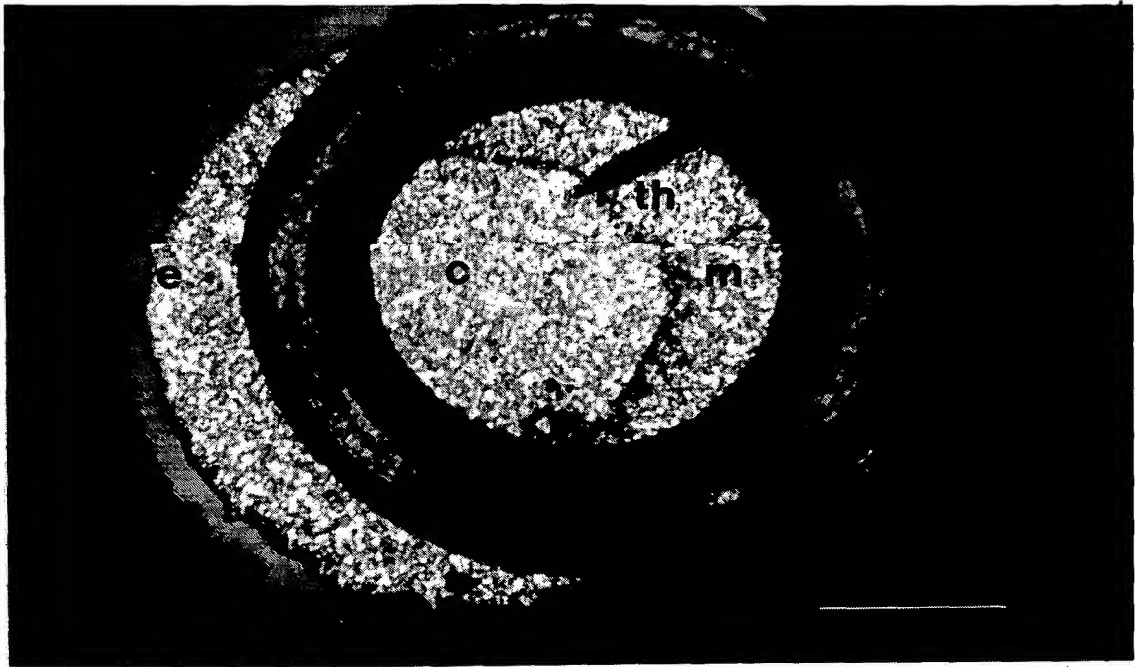


Fig. 8.1a

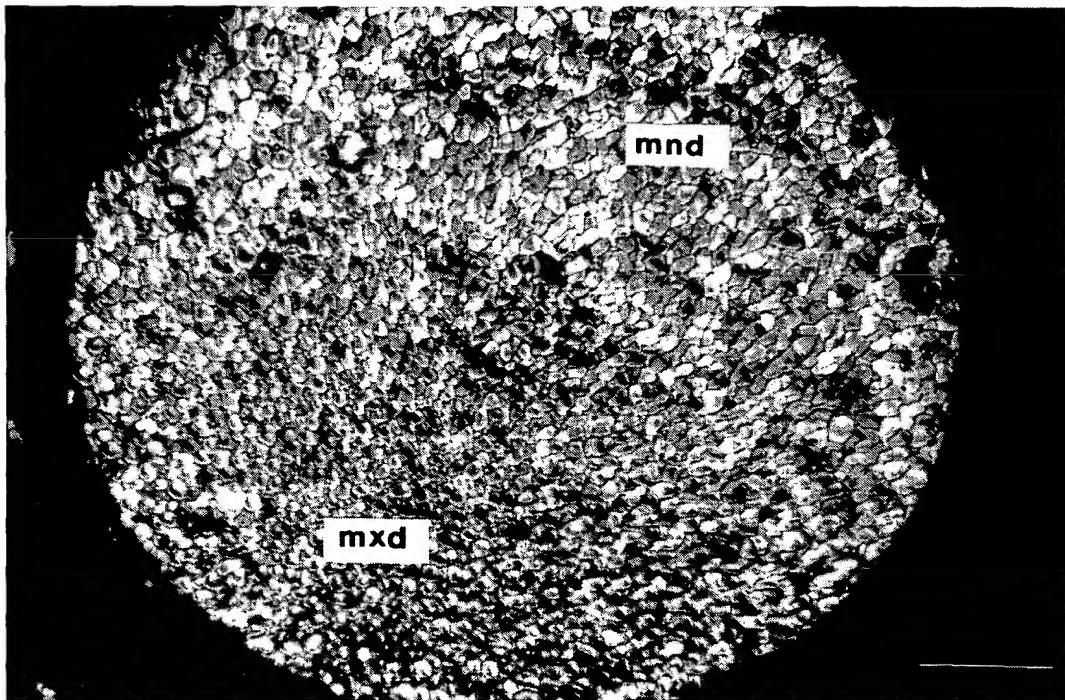
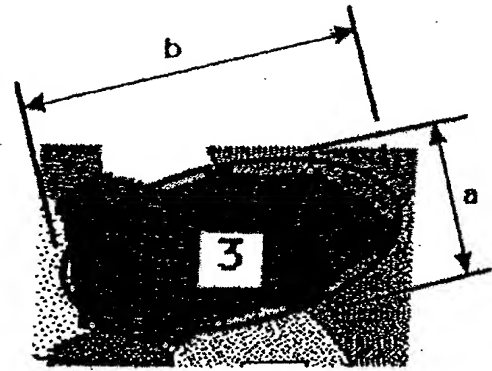
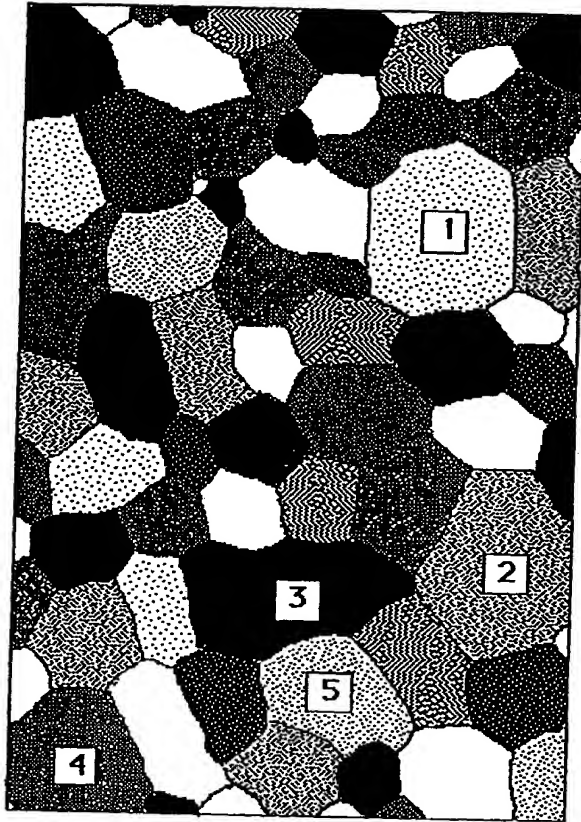


Fig. 8.1b

09875348.01260
202210.8459/860



grain area = $0.25ab$

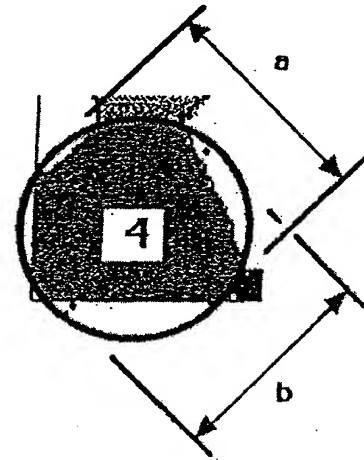


Fig. 8.2

203270" SHE92060

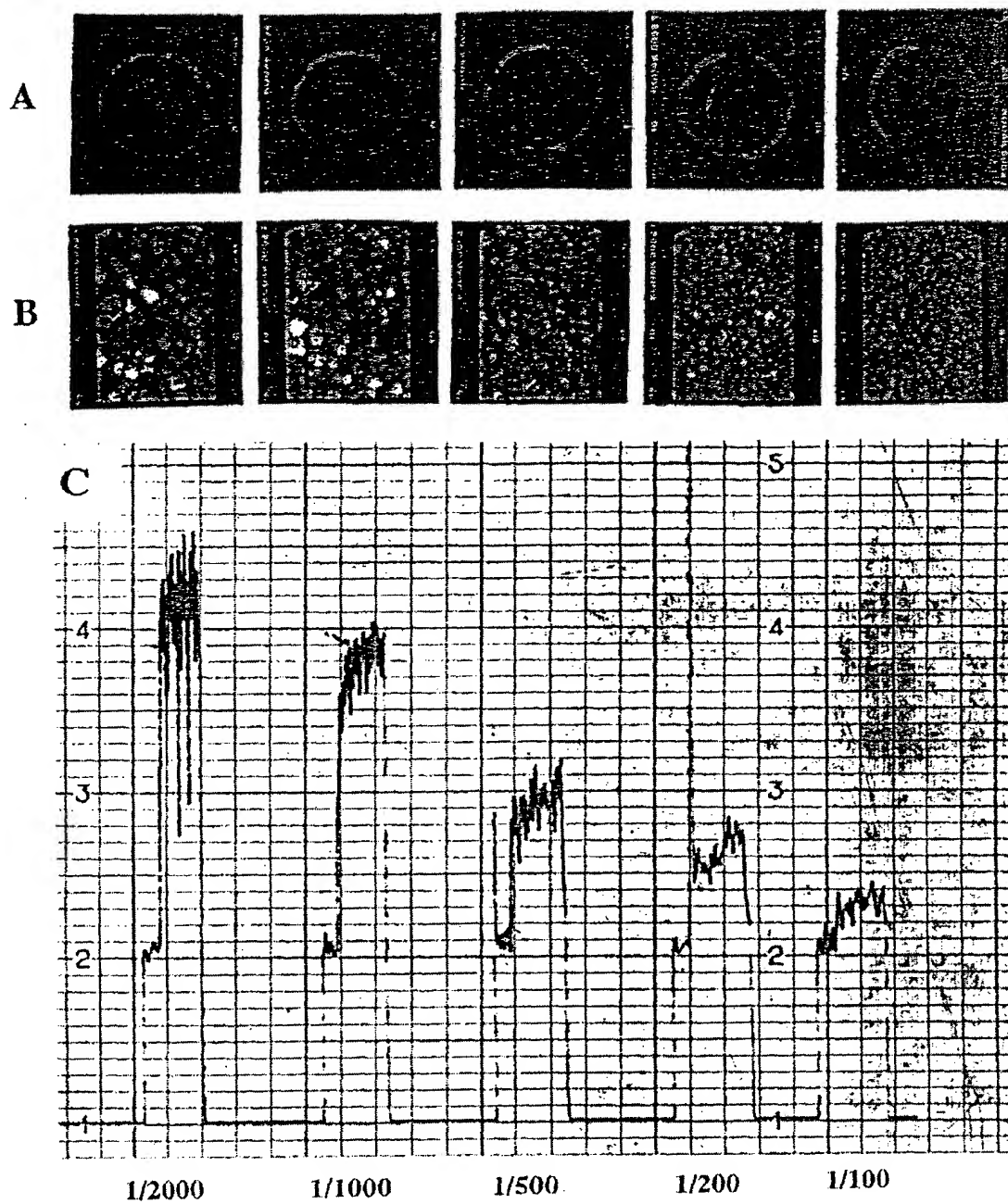


Fig. 8.3

2025-01-09 09:29:00

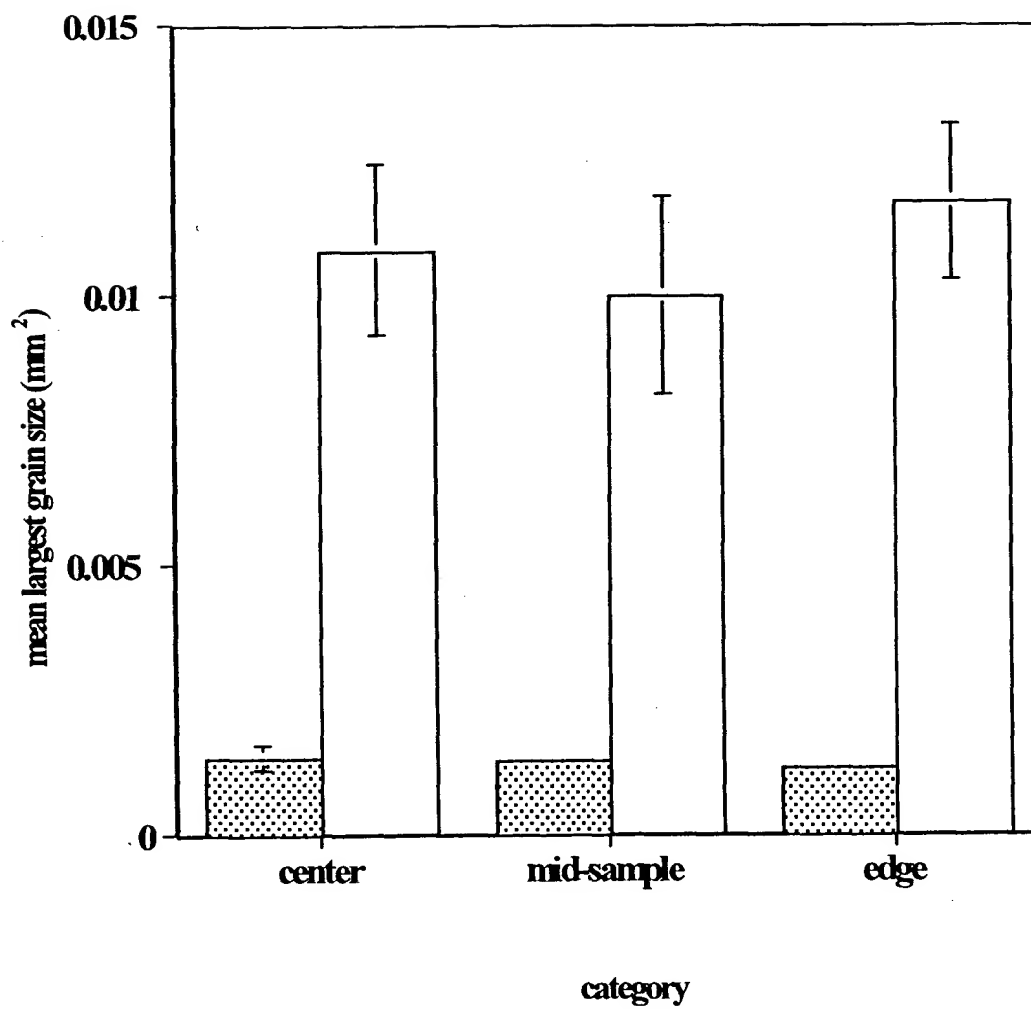


Fig. 8.4a

A

B

Fig. 8.4b

000000 01092860

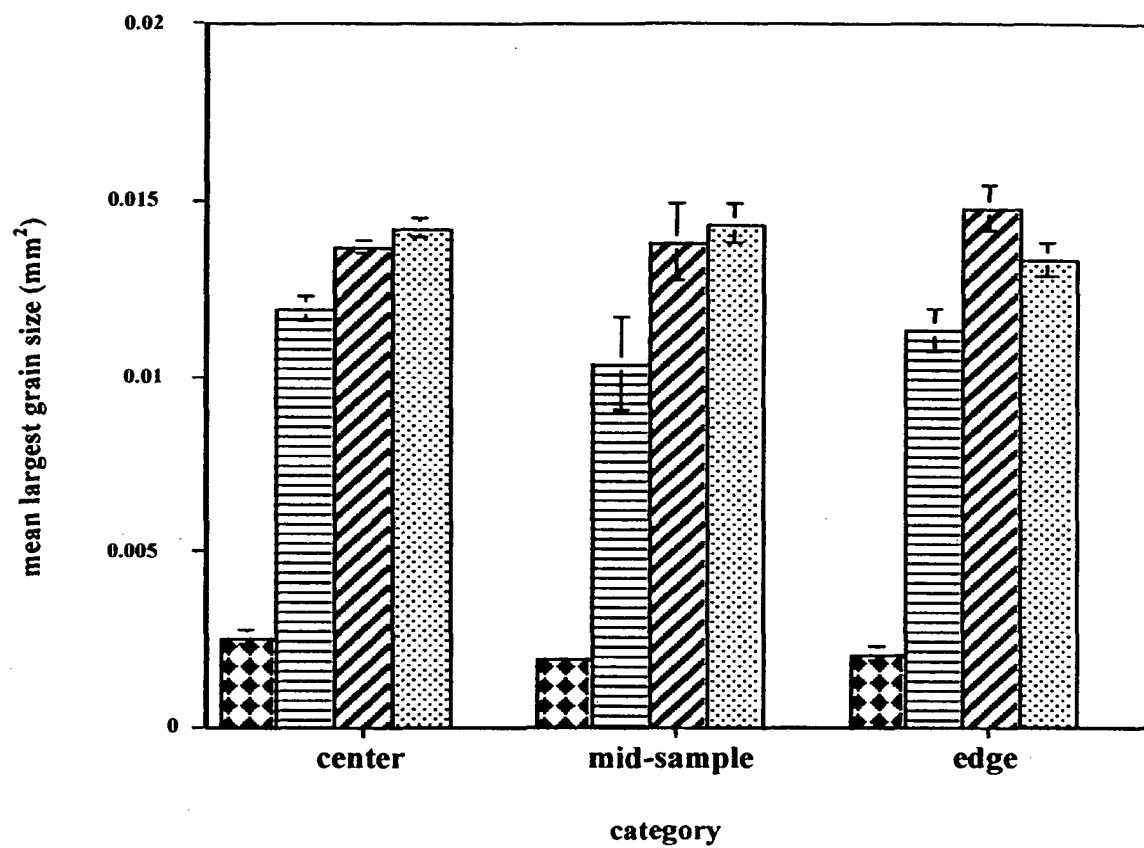


Fig. 8.5a

203210" BH29/2560

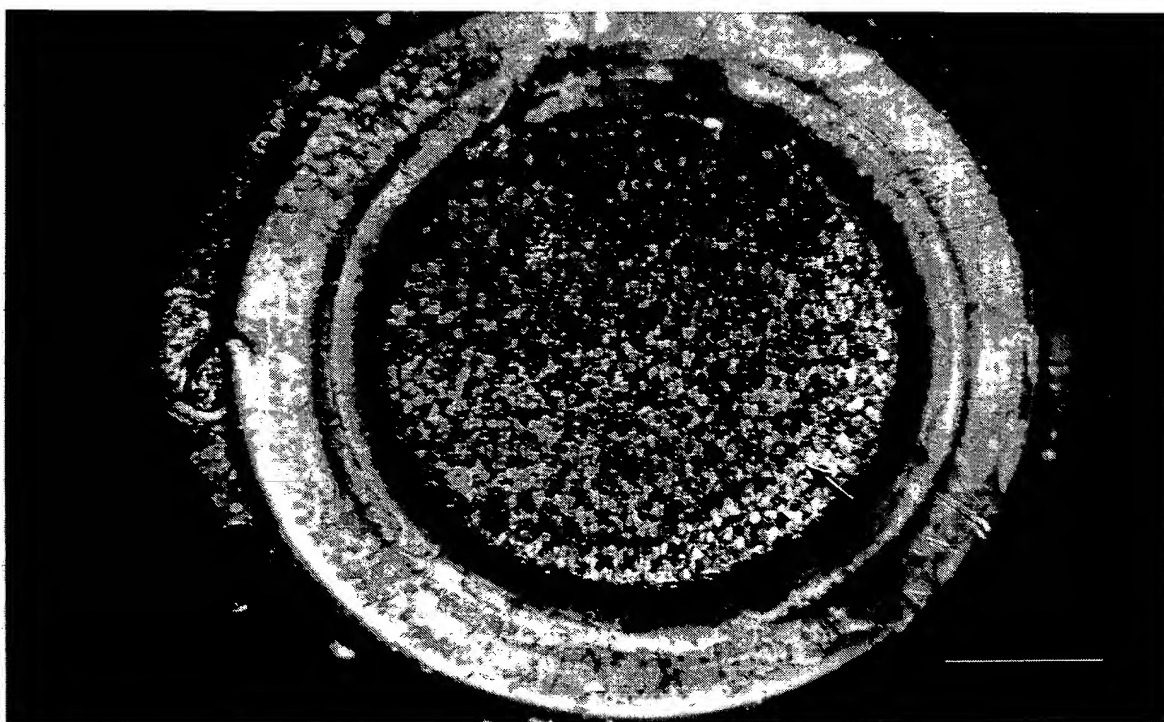


Fig. 8.5b

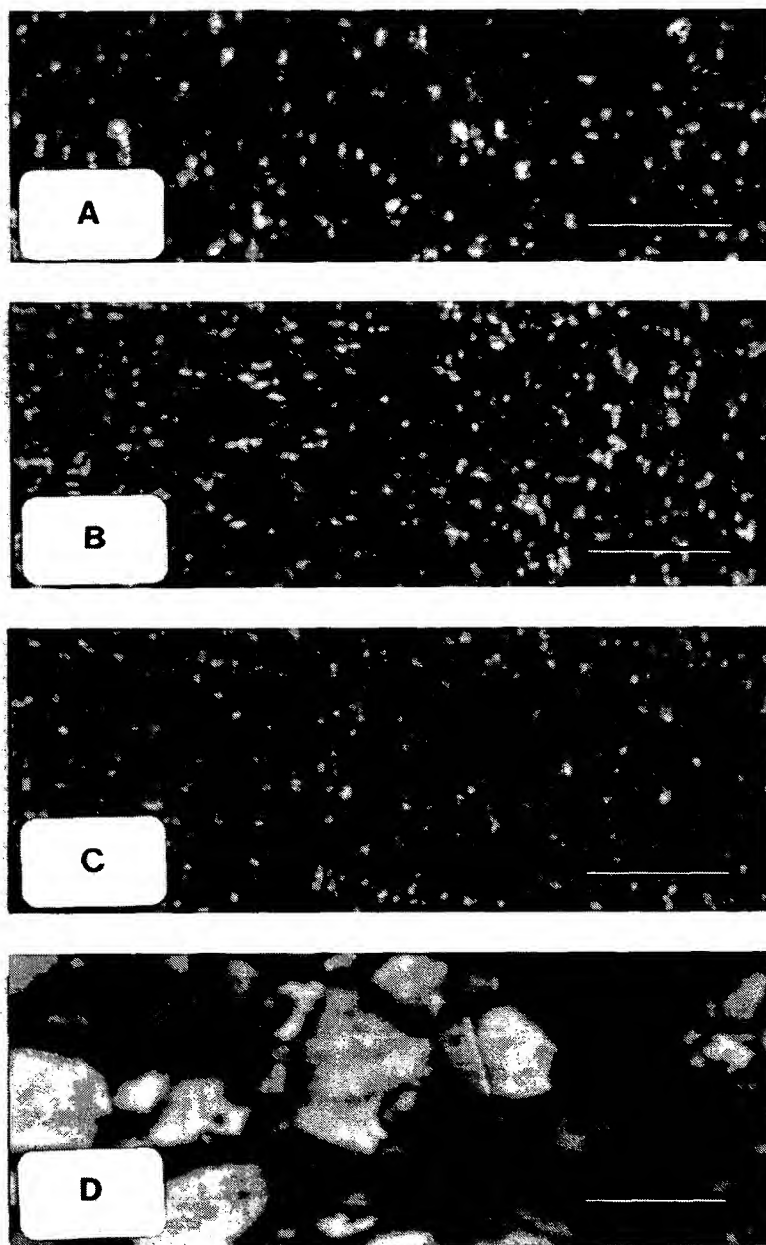


Fig. 8.6

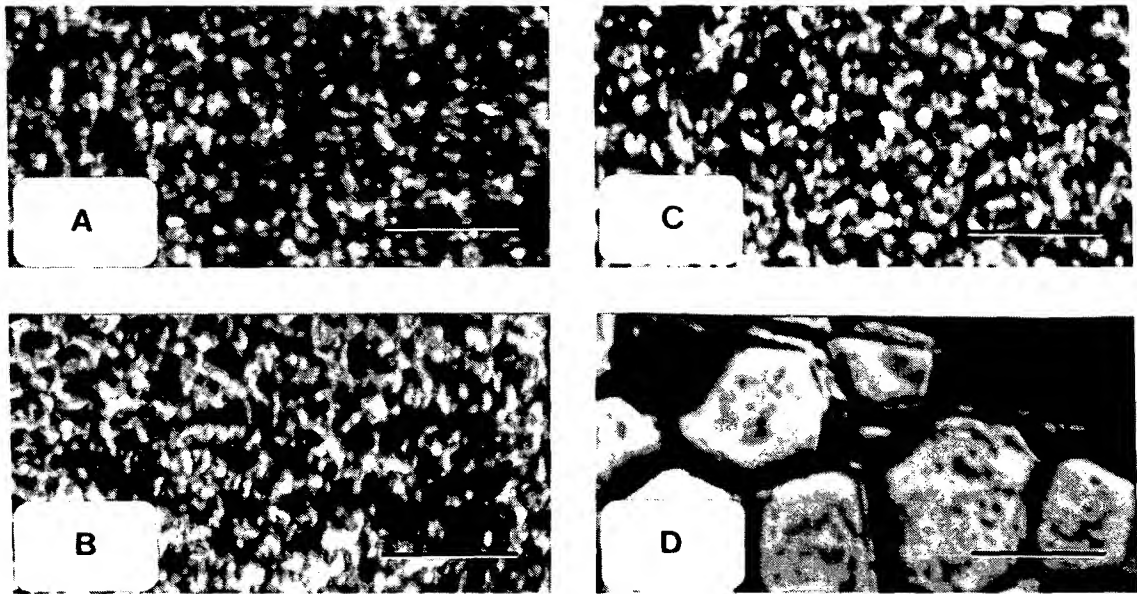


Fig. 8.7

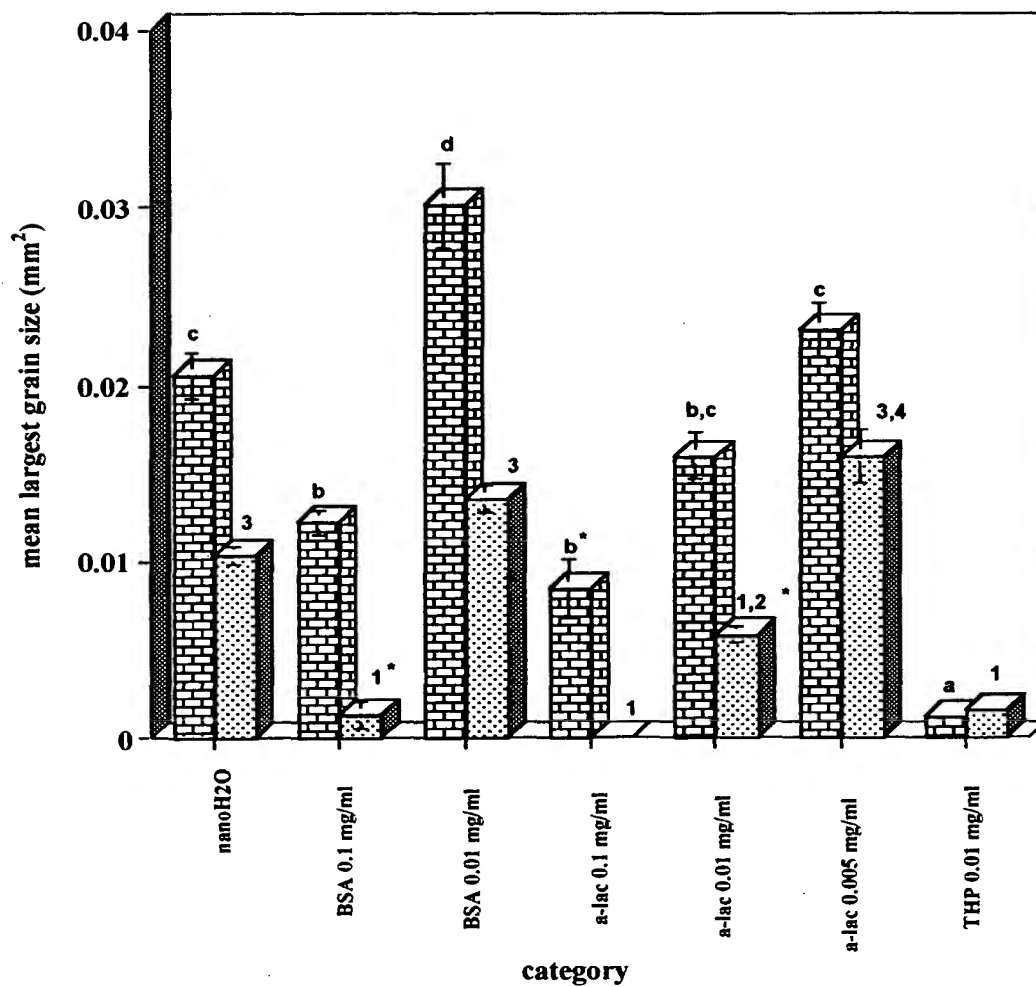


Fig. 8.8

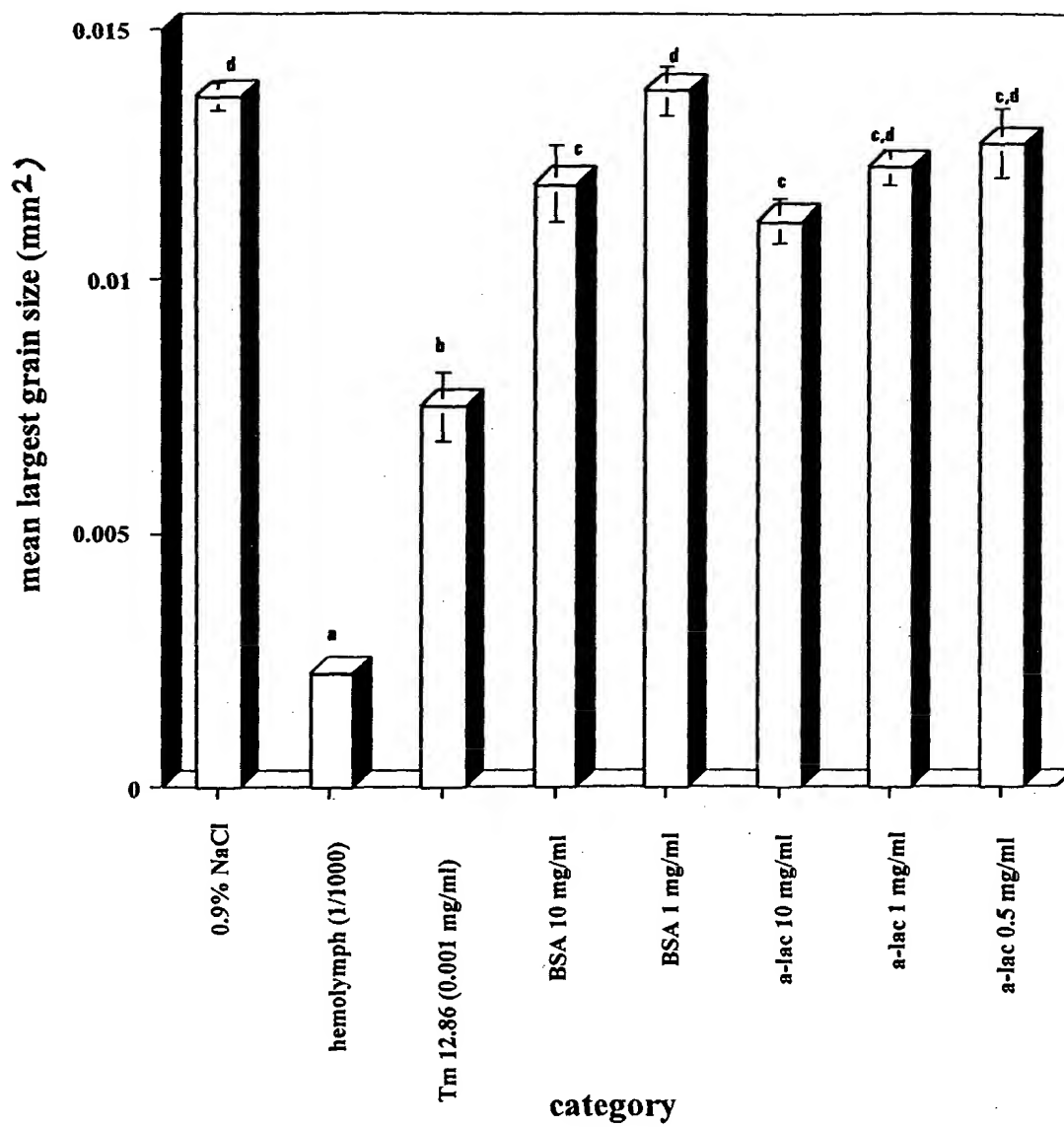


Fig. 8.9

2025031200

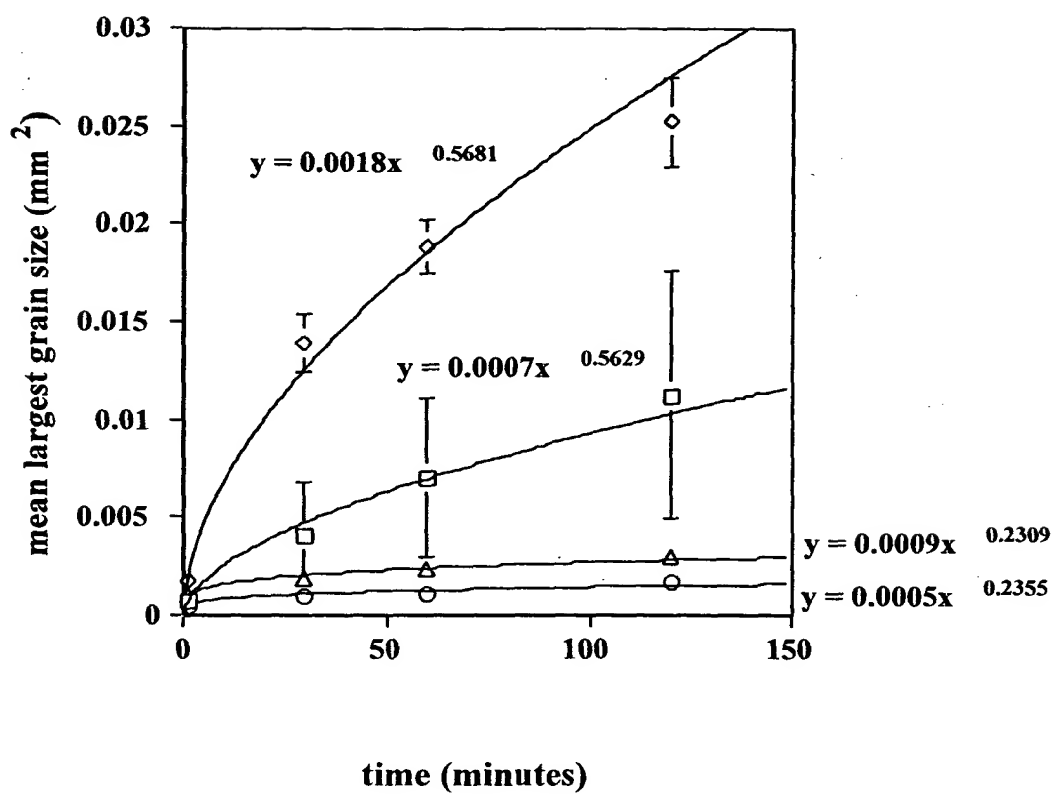


Fig. 8.10

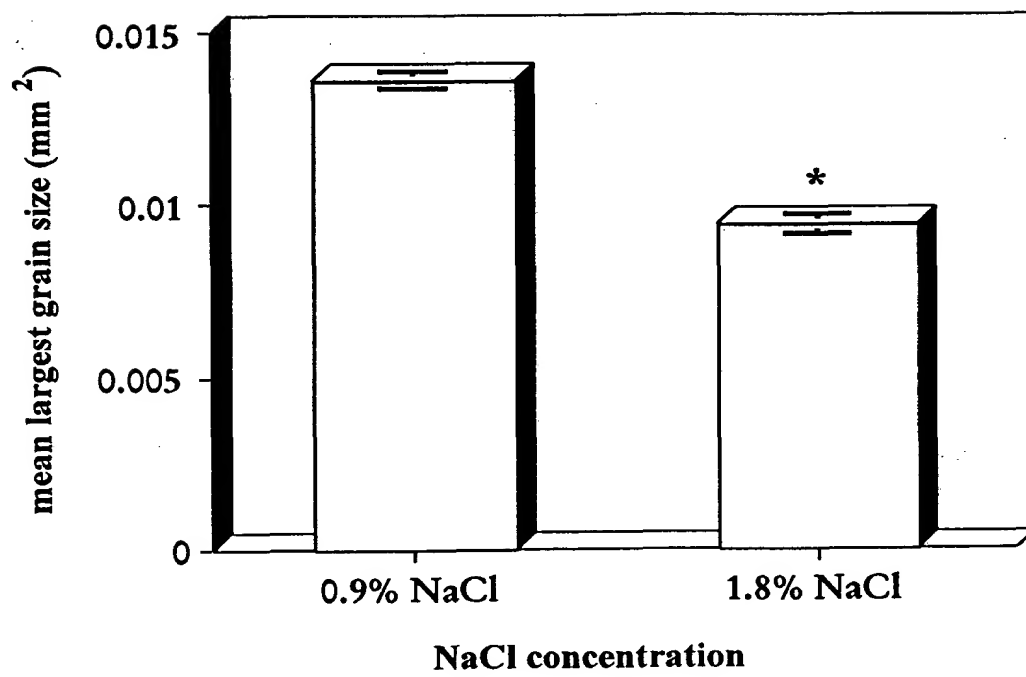
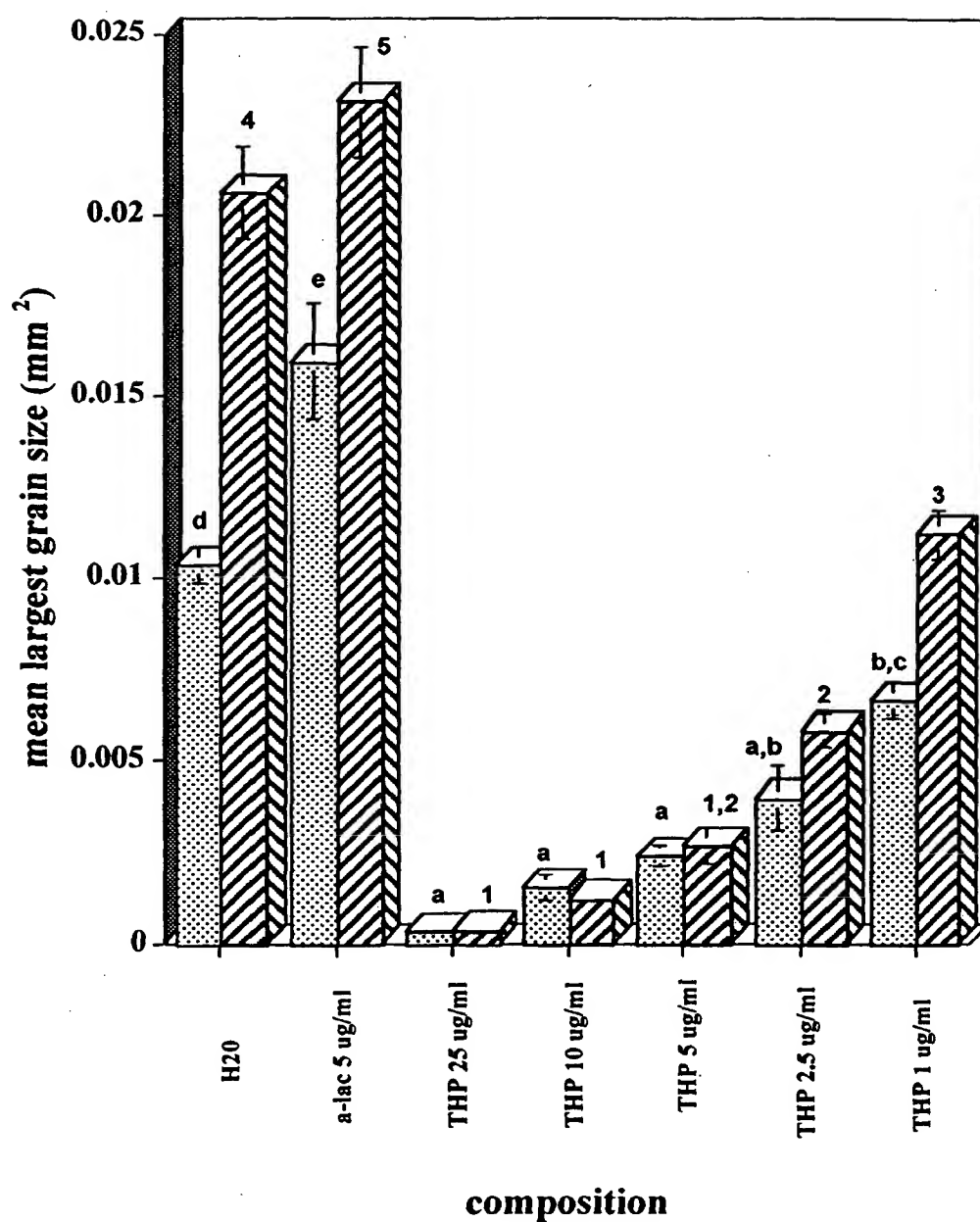


Fig. 8.11

Figure 1 consists of six panels, A through F, showing electron micrographs of the developing chick retina. Panels A through E are arranged vertically on the left, showing a progression from early to late stages of retinal development. Panel F is on the right, showing a higher magnification view of the photoreceptor layer. Each panel includes a scale bar in the bottom right corner.

Fig. 8.12

*Fig. 8.13*

200270 0152860

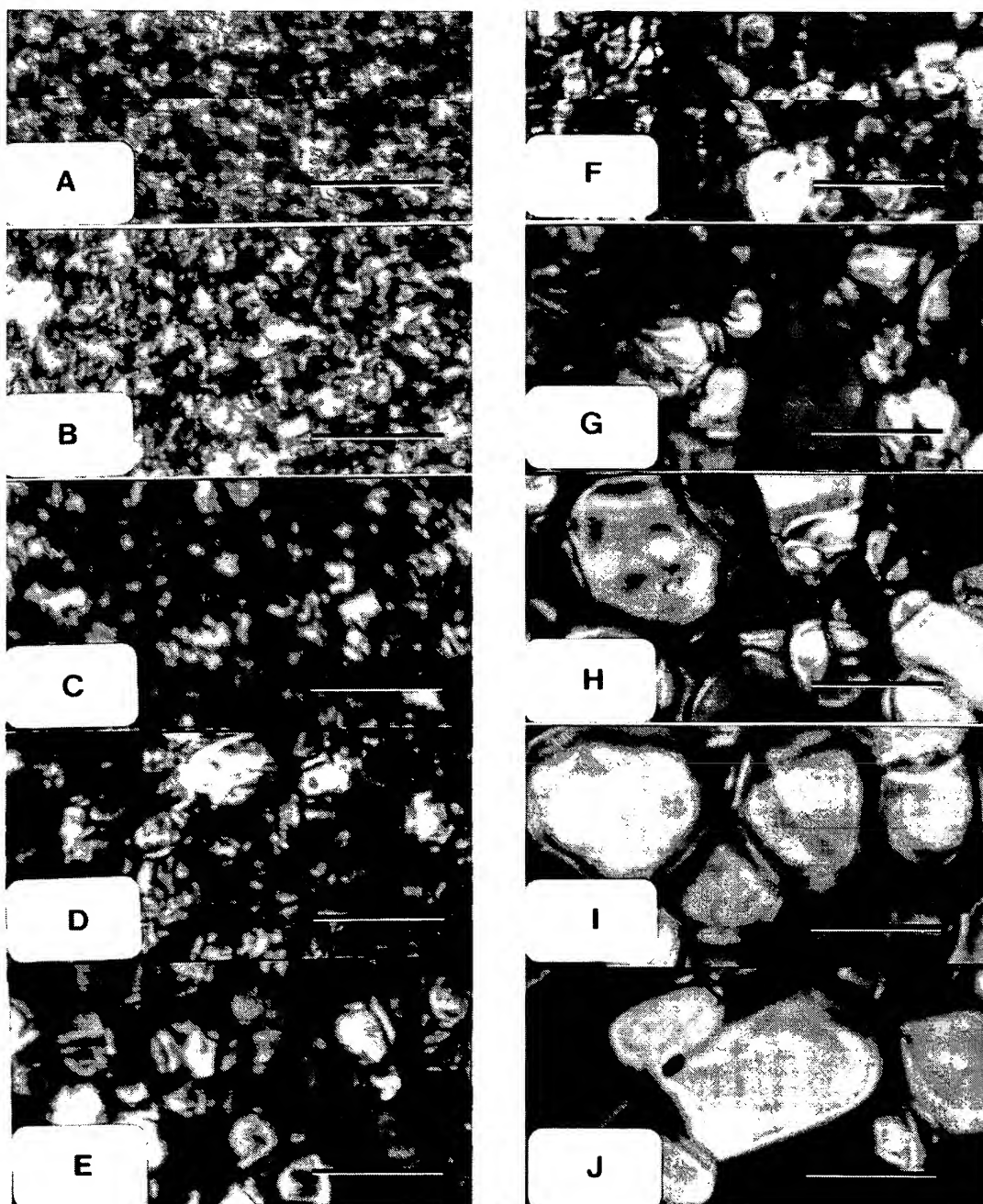


Fig. 8.14

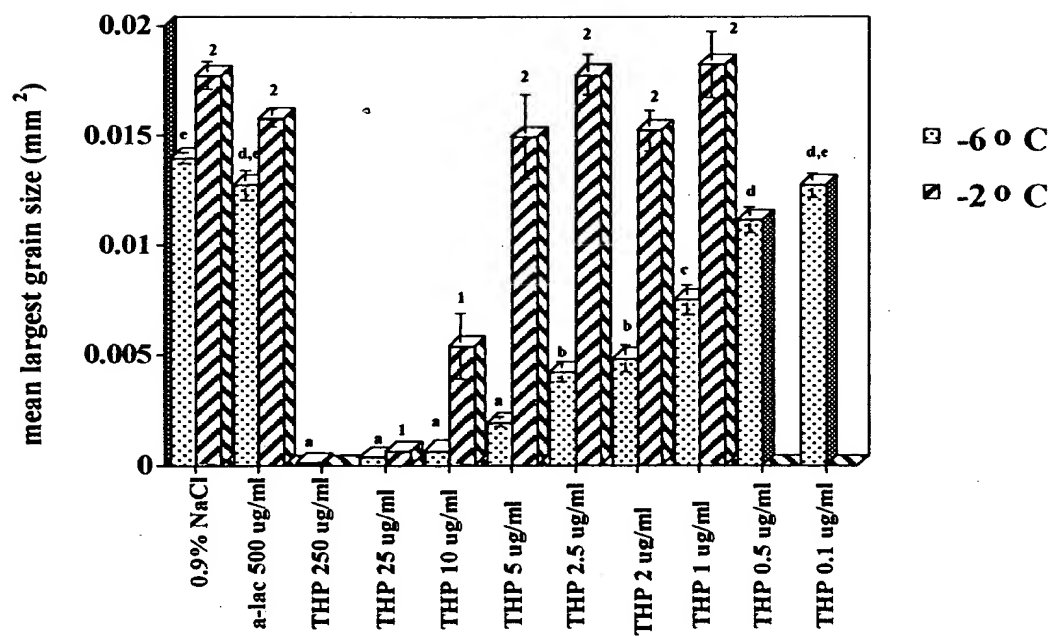


Fig. 8.15

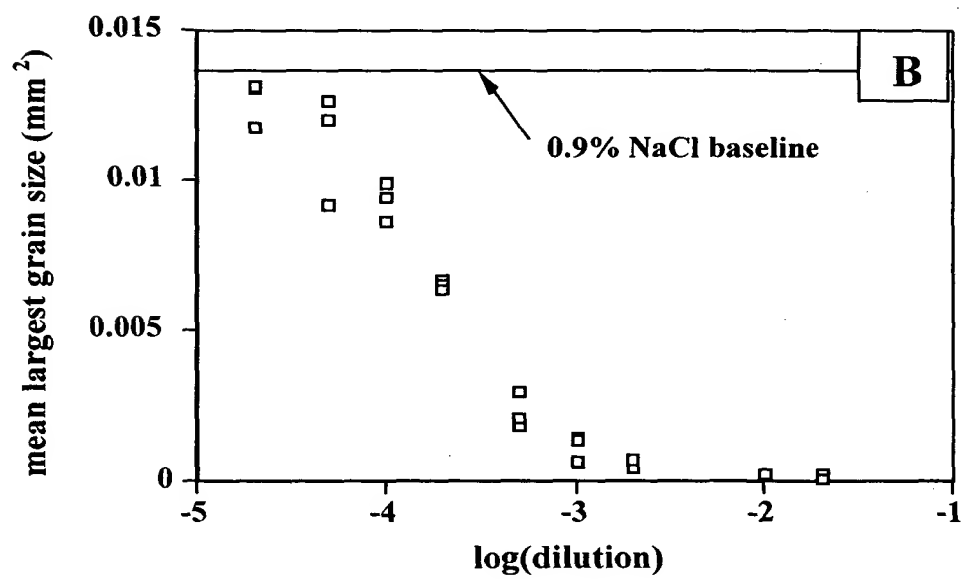
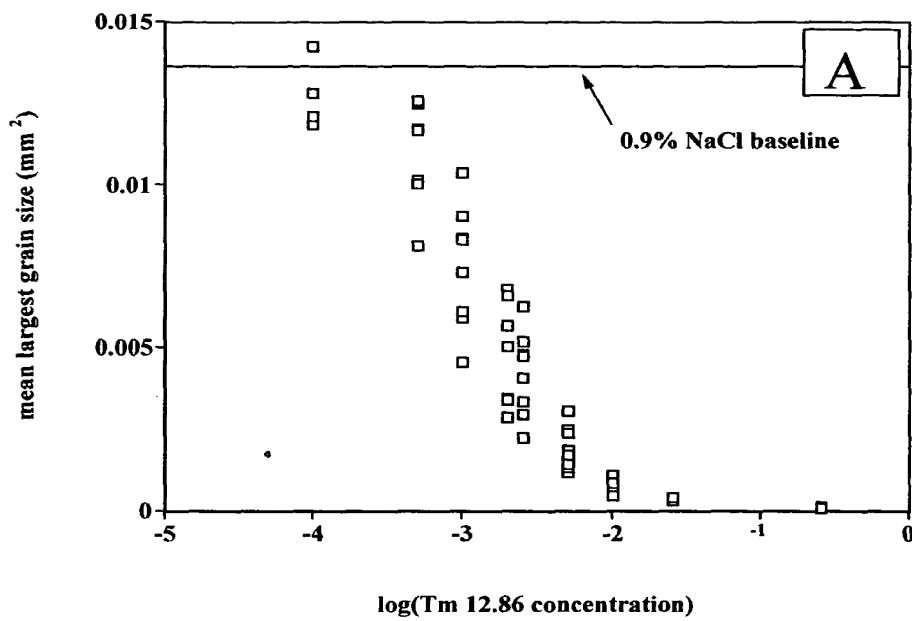


Fig. 8.16

000000 000000 000000

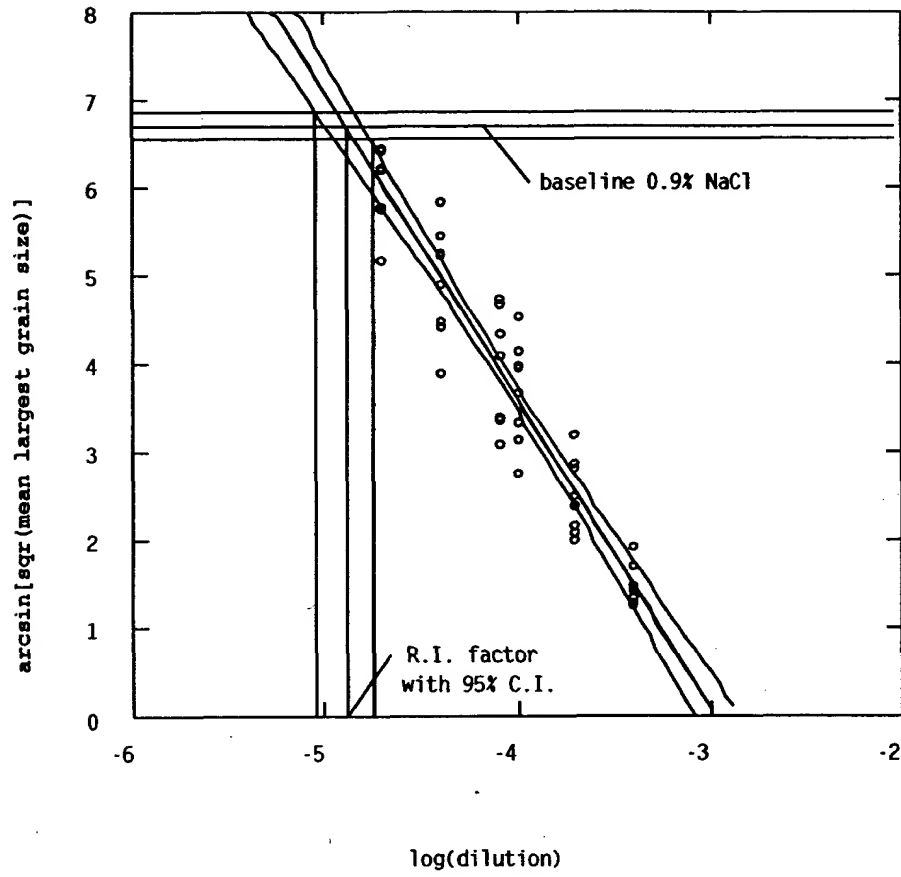


Fig. 8.18

202510 01492860

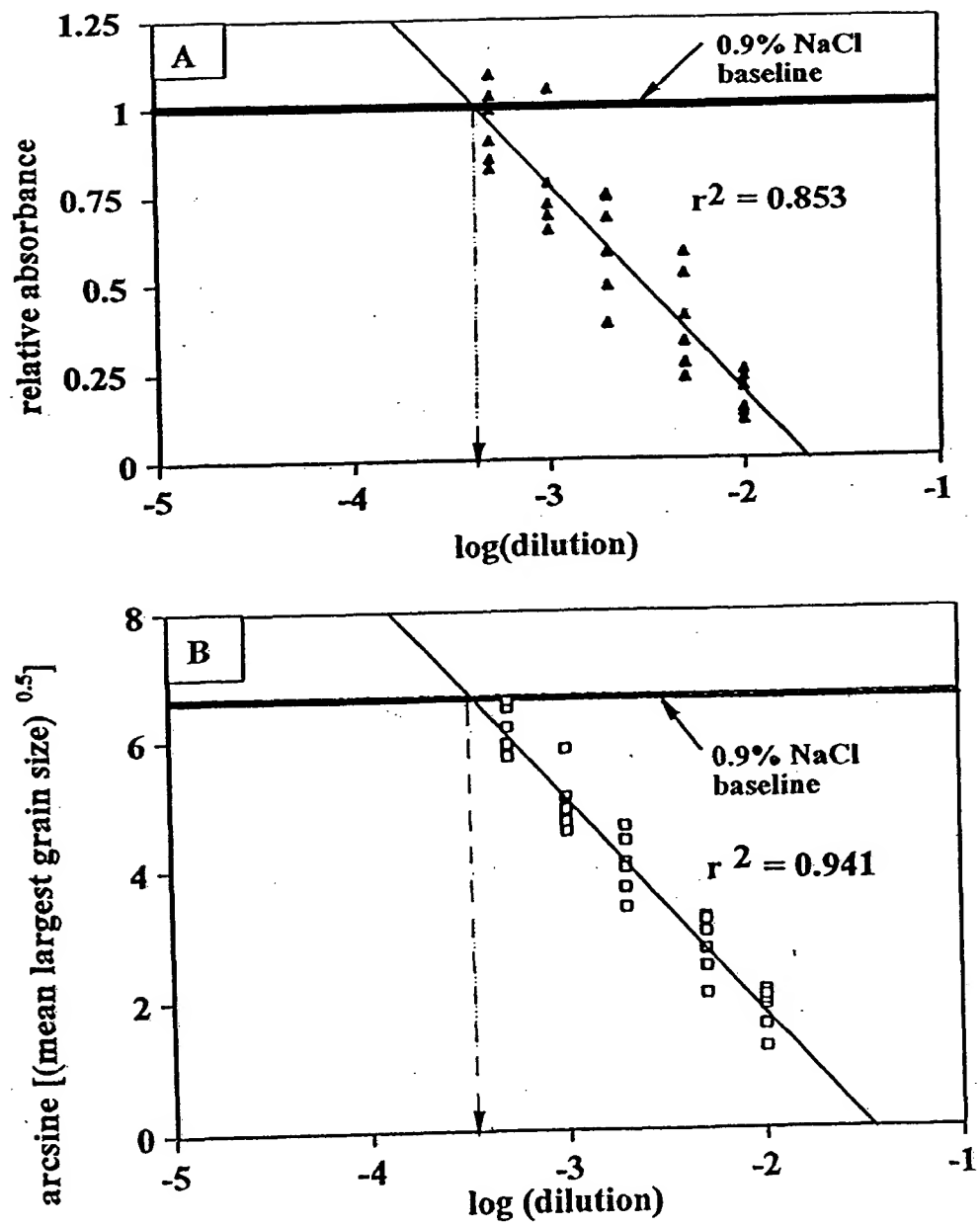


Fig. 8.19

2025-09-20 14:28:00

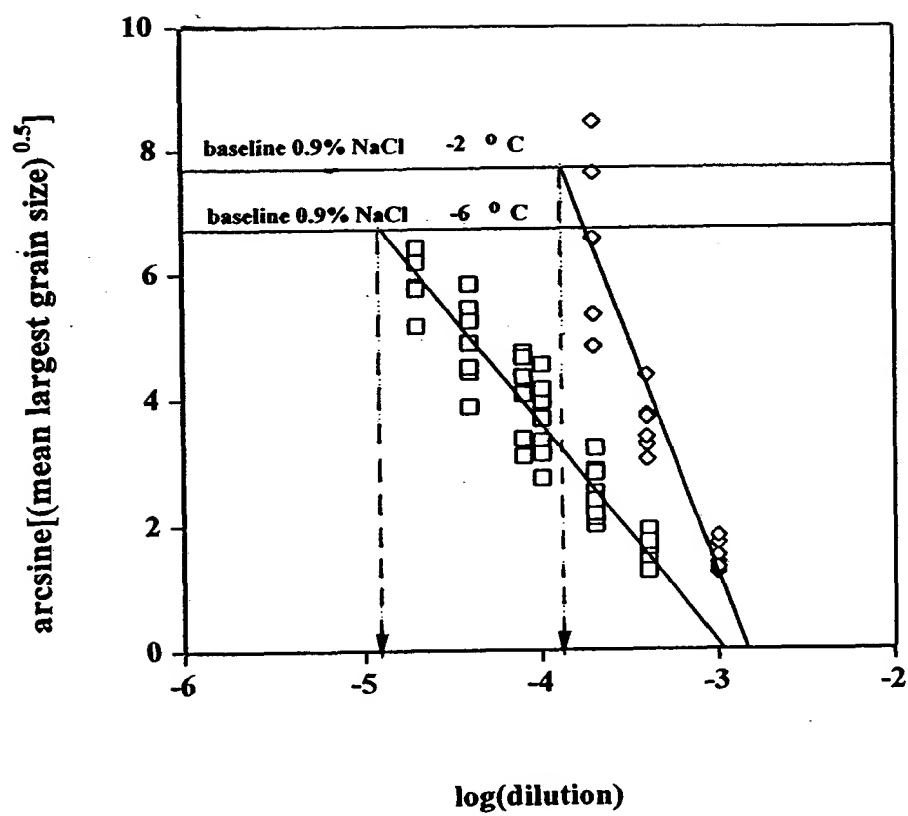


Fig. 8.20

20250101 09:20:00

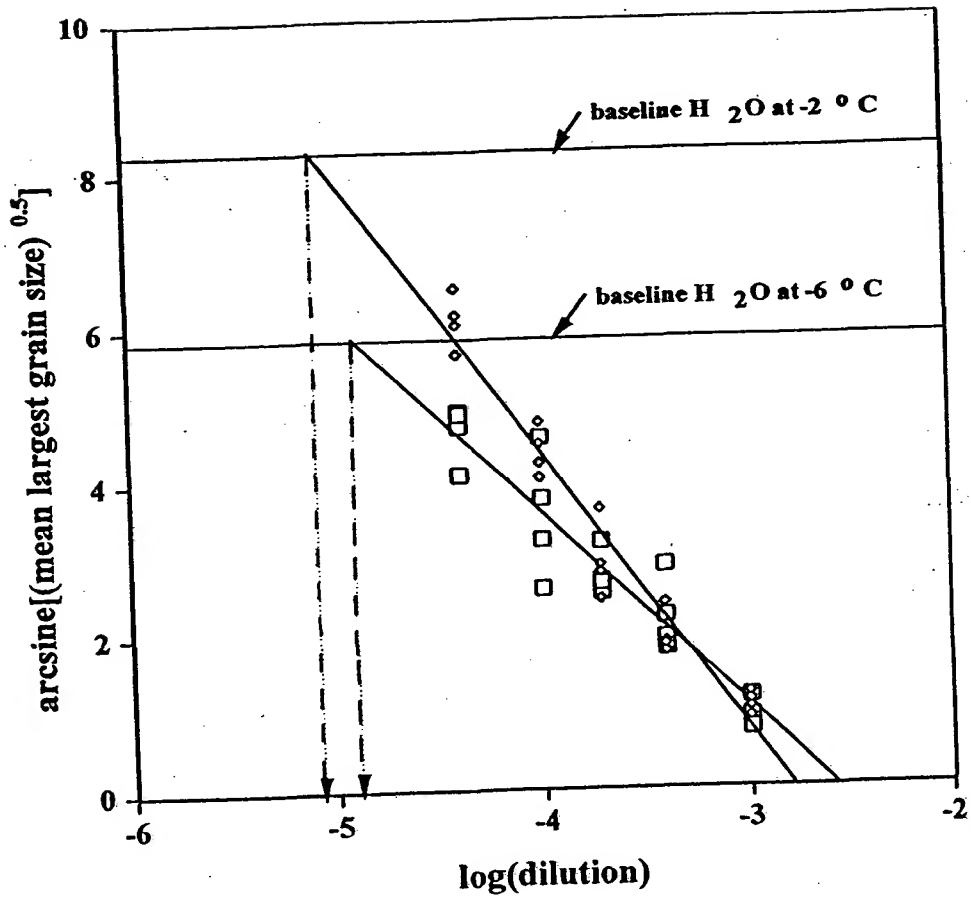


Fig. 8.21

202210 01492560

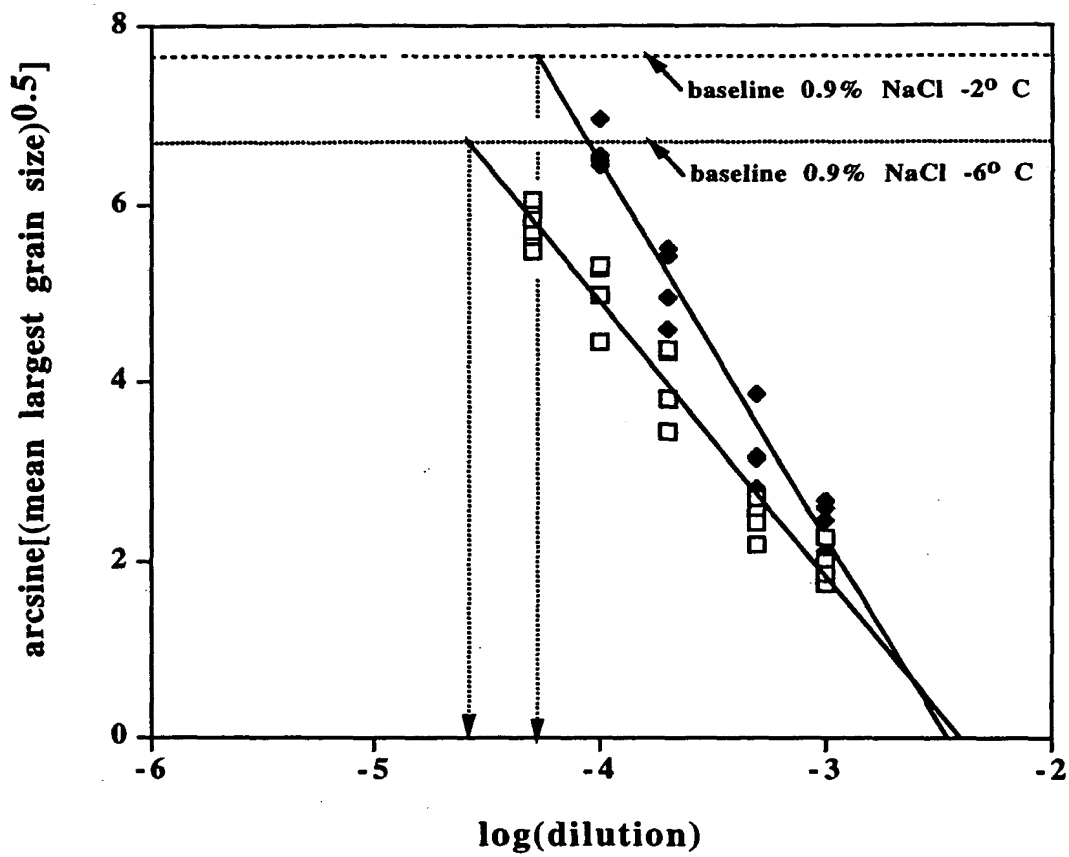


Fig. 8.22

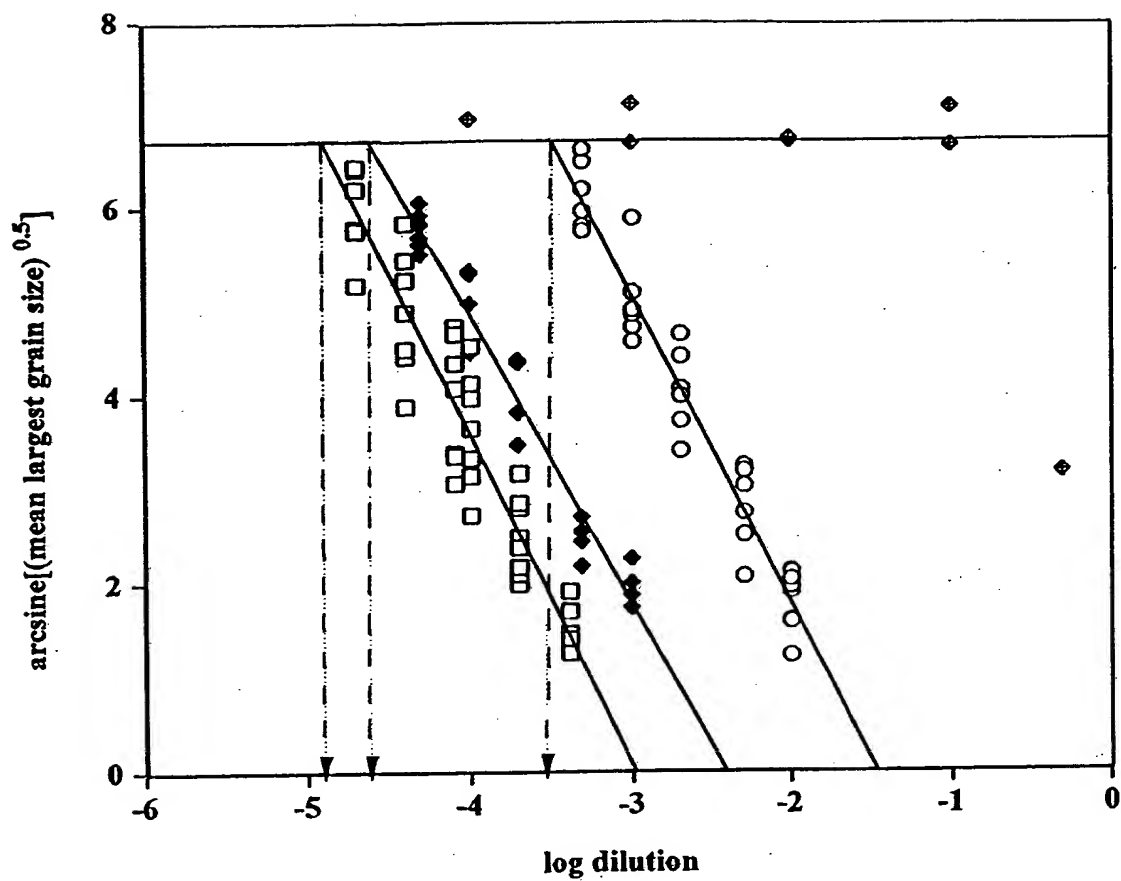


Fig. 8.23

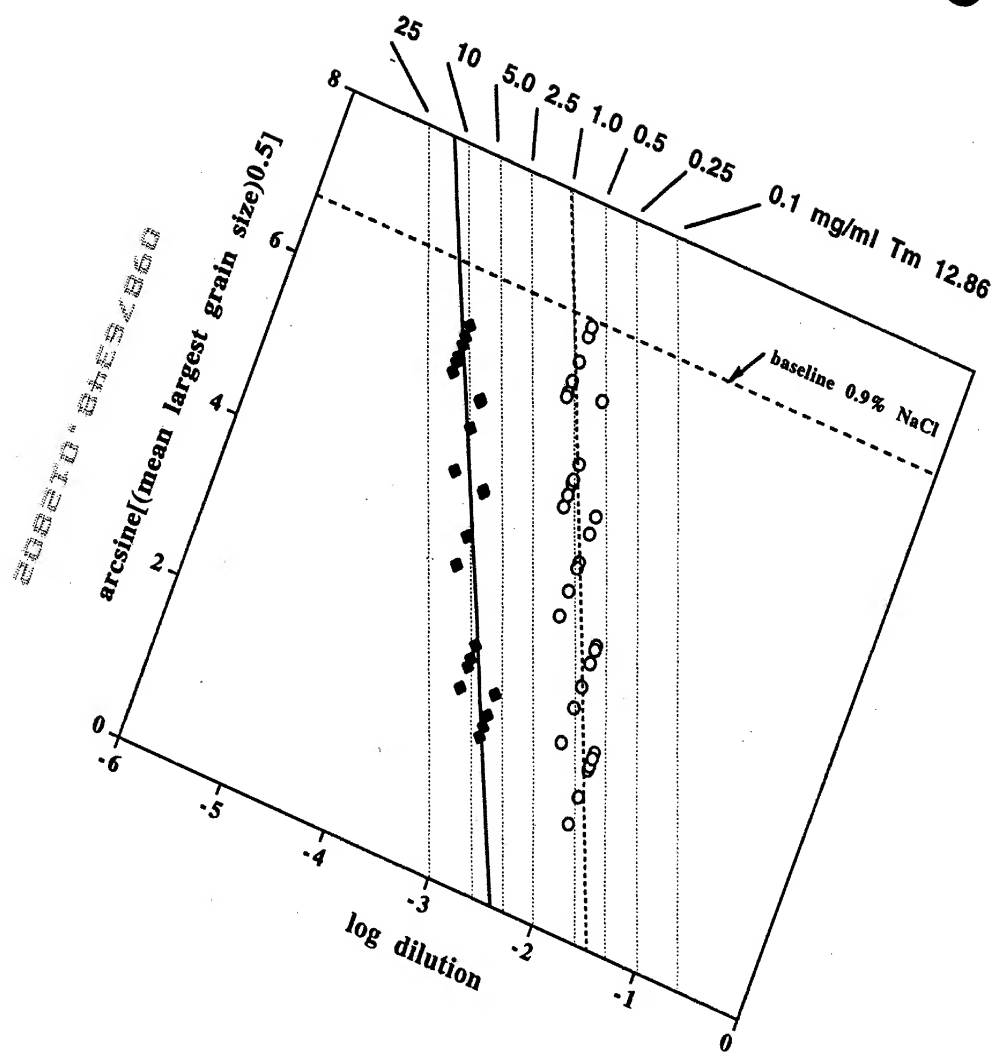


Fig. 8.24

203210 315/960

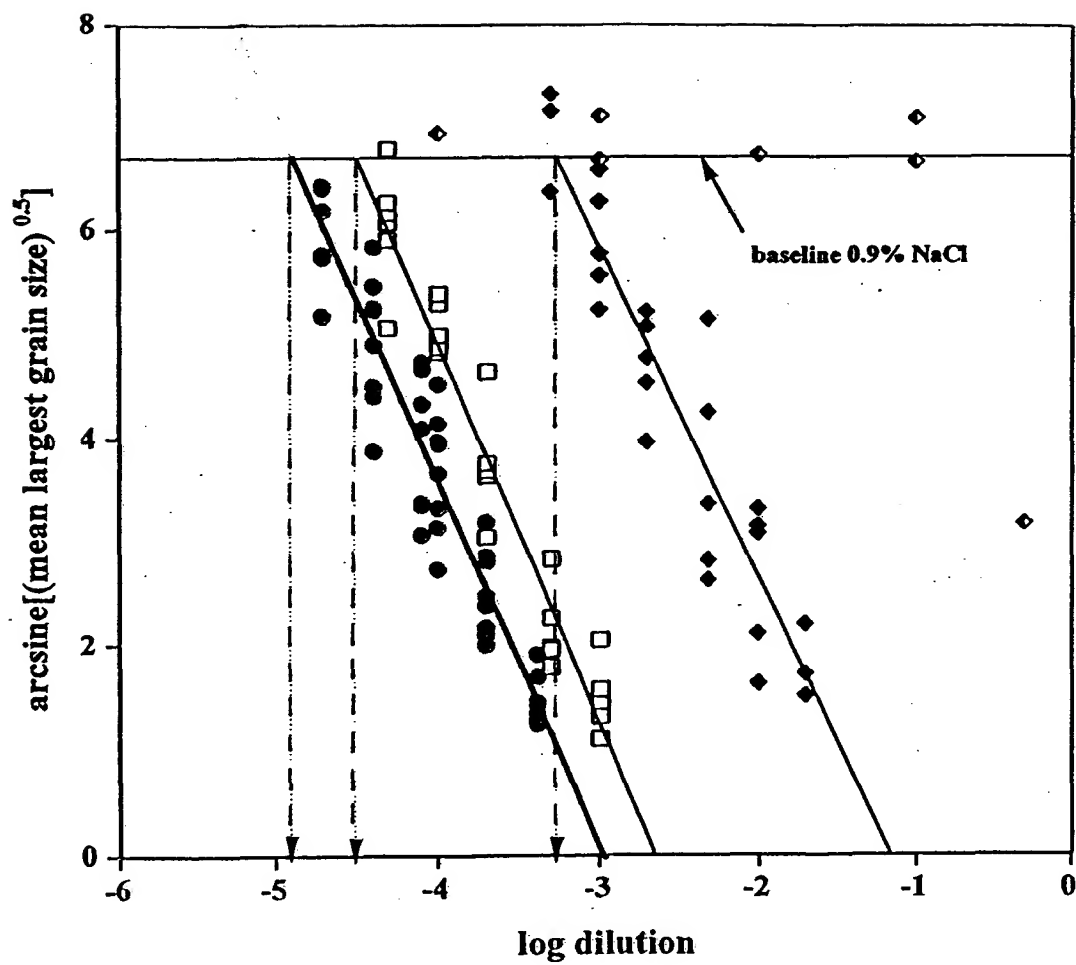


Fig. 8.25

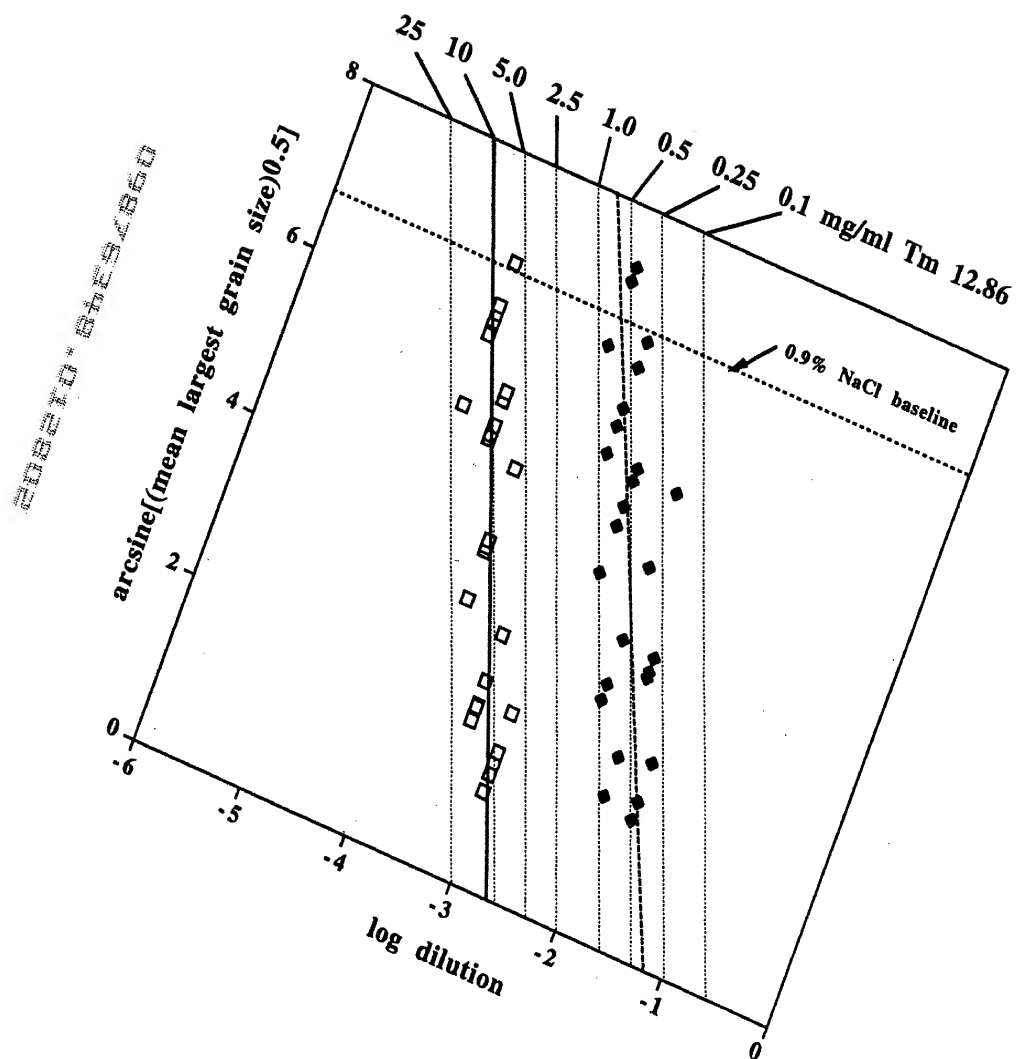


Fig. 8.26

200270 31254860

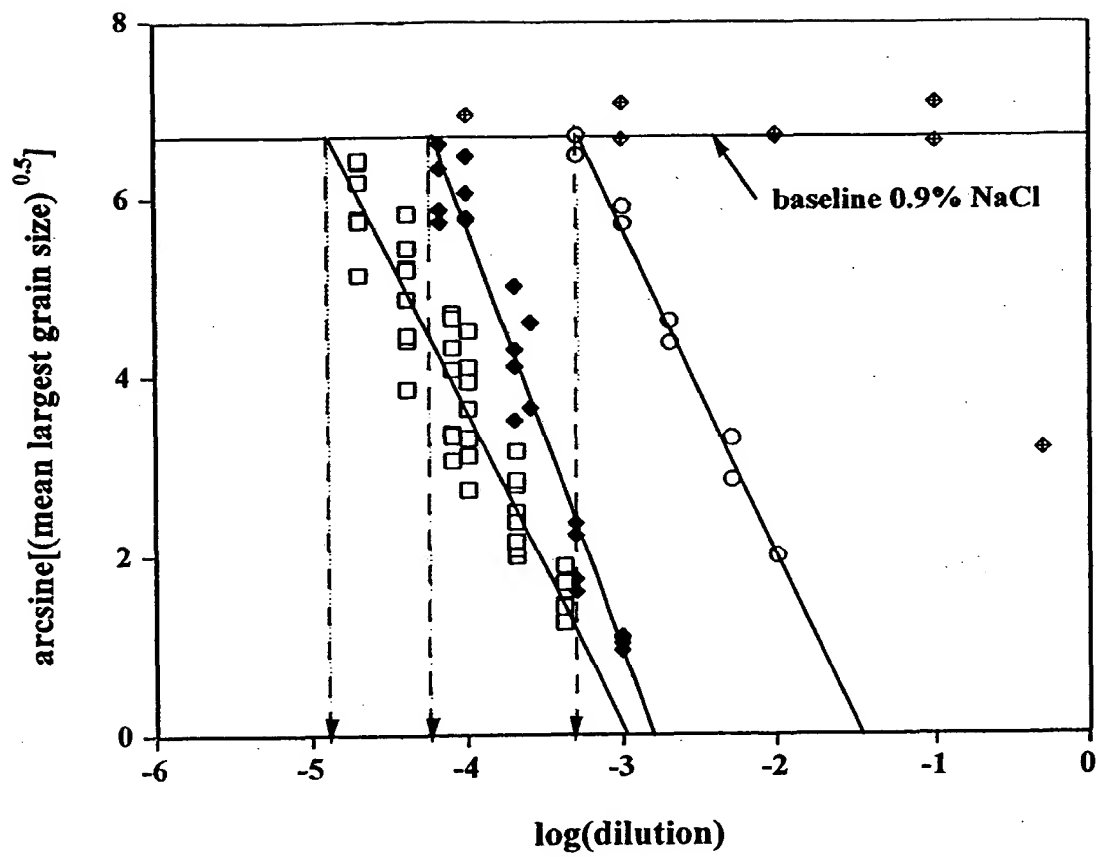


Fig. 8.27

2025-07-01 09:28:28

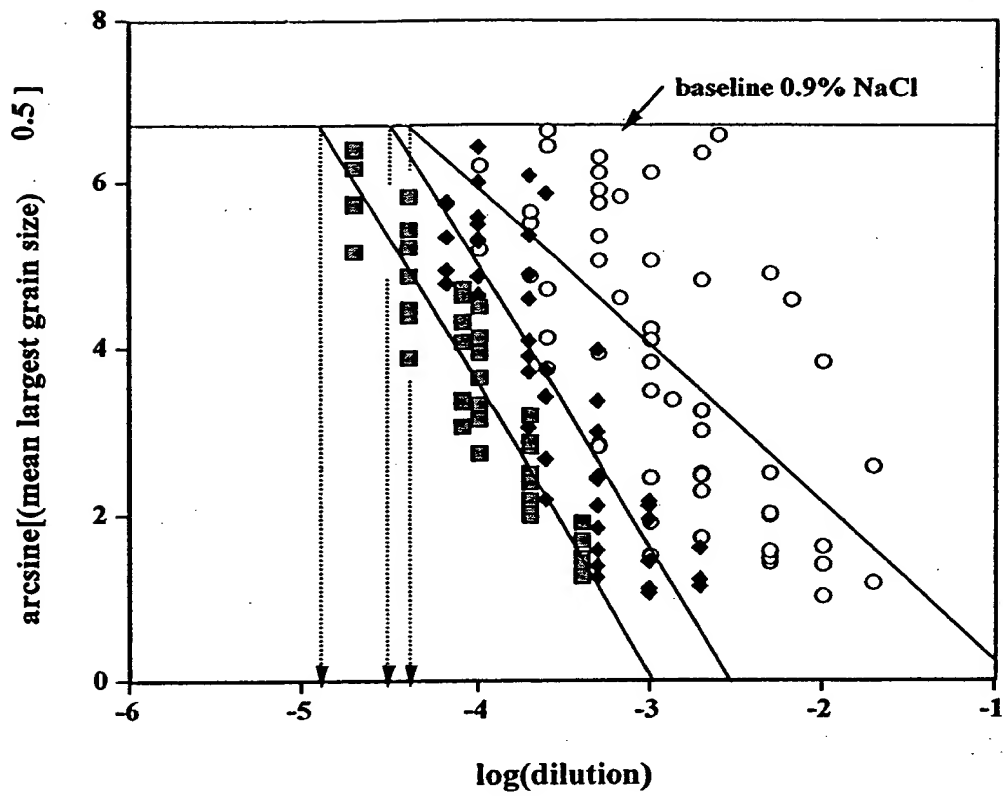


Fig. 8.28

002210 0123456789

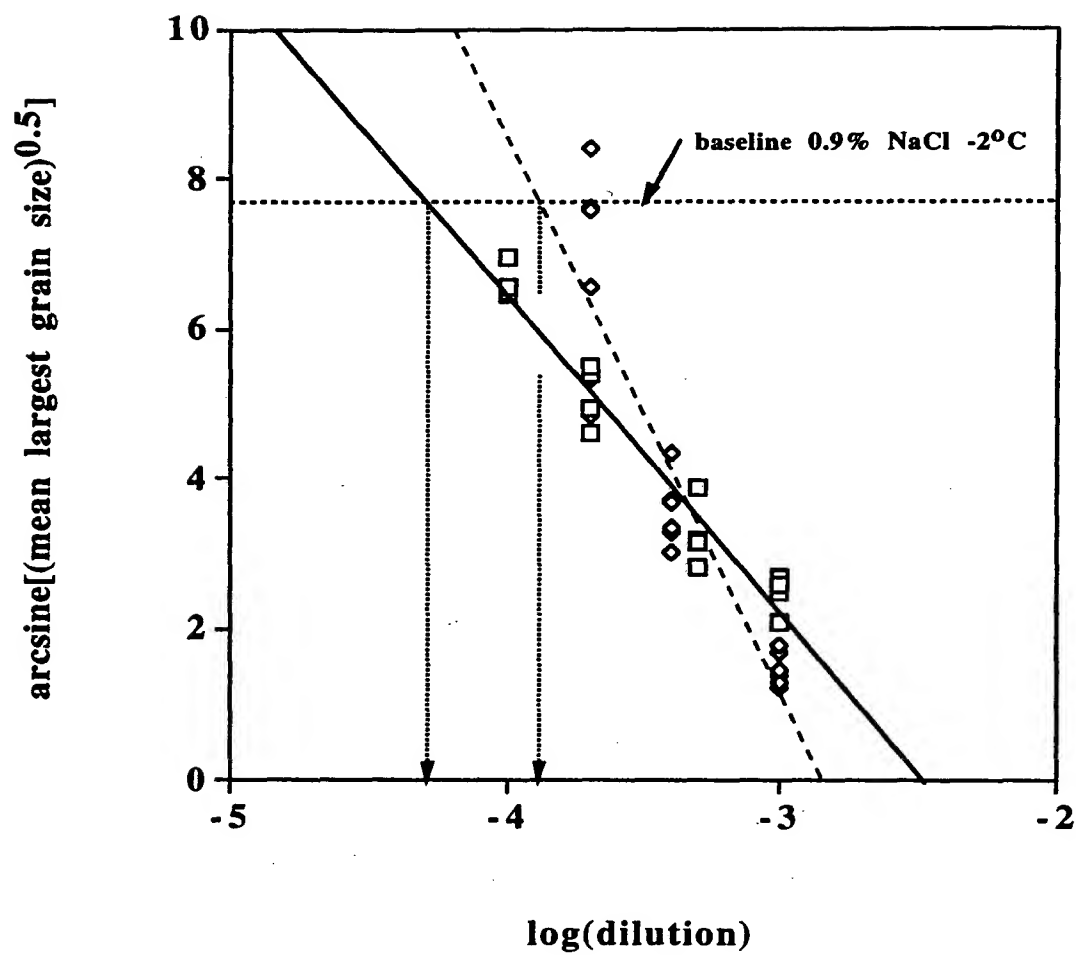


Fig. 8.29

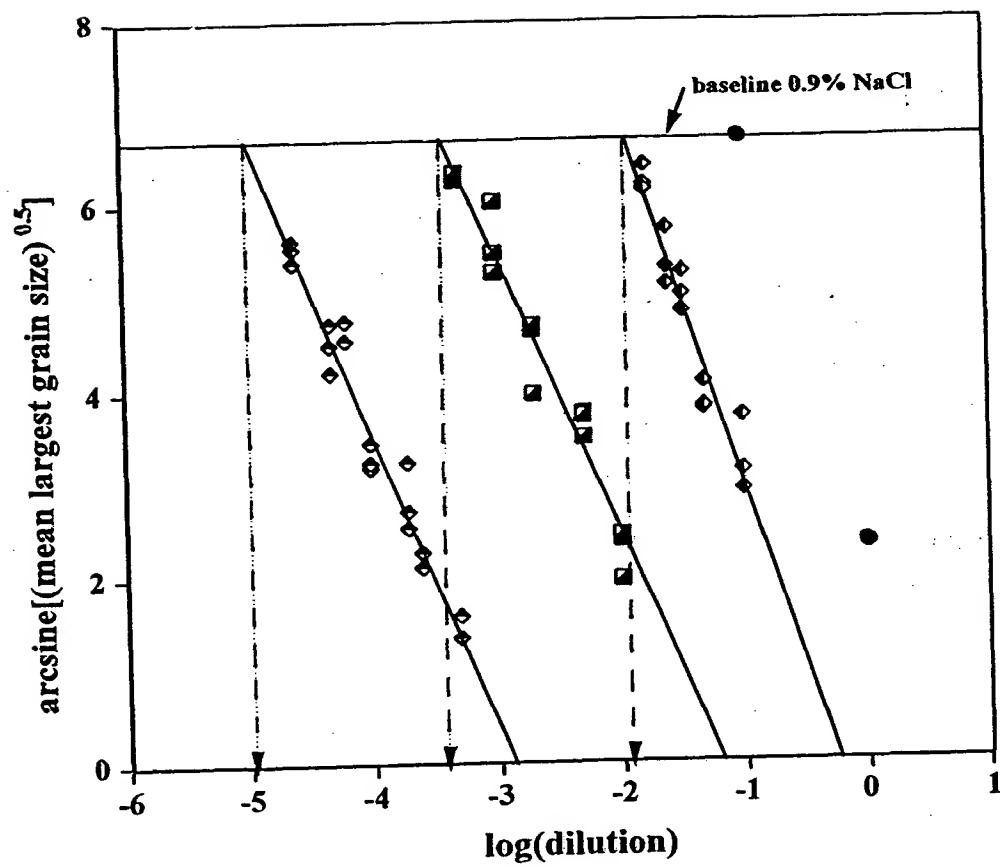


Fig. 8.30

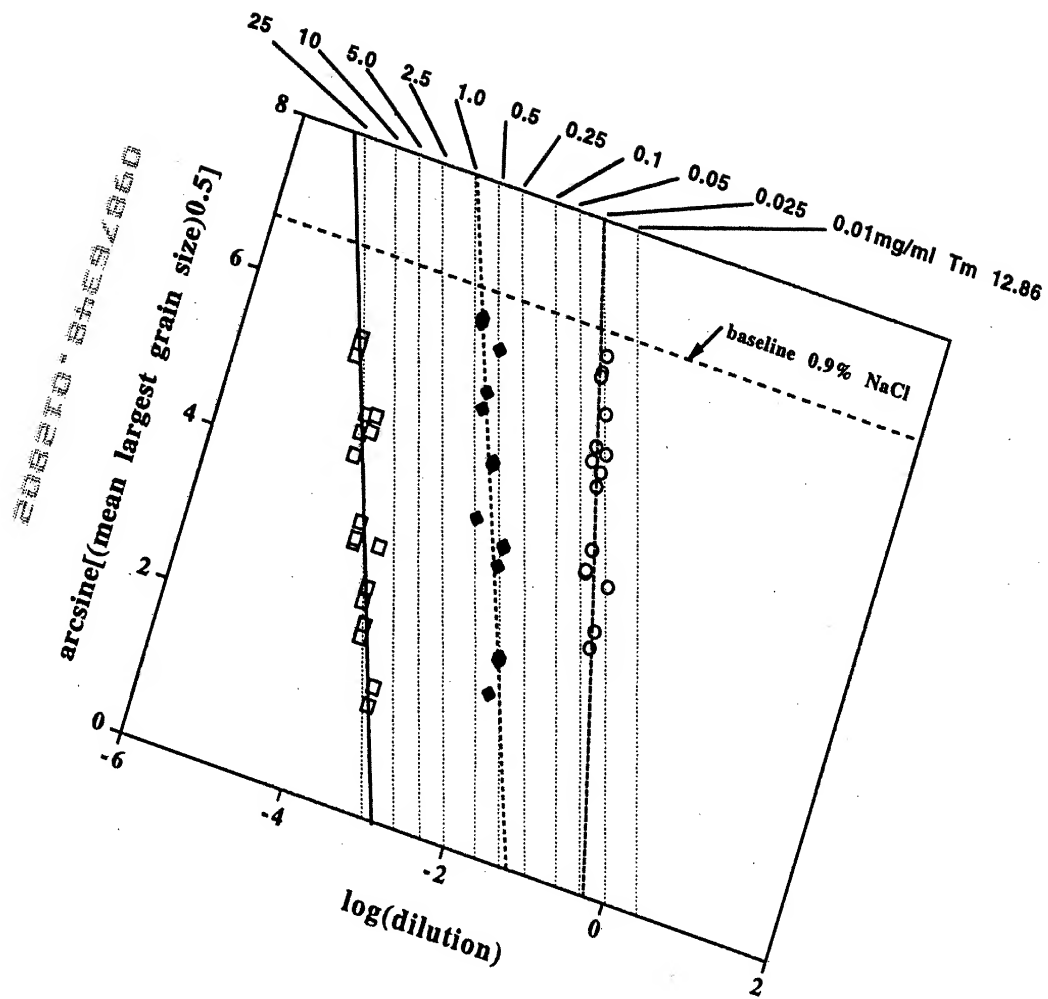


Fig. 8.31

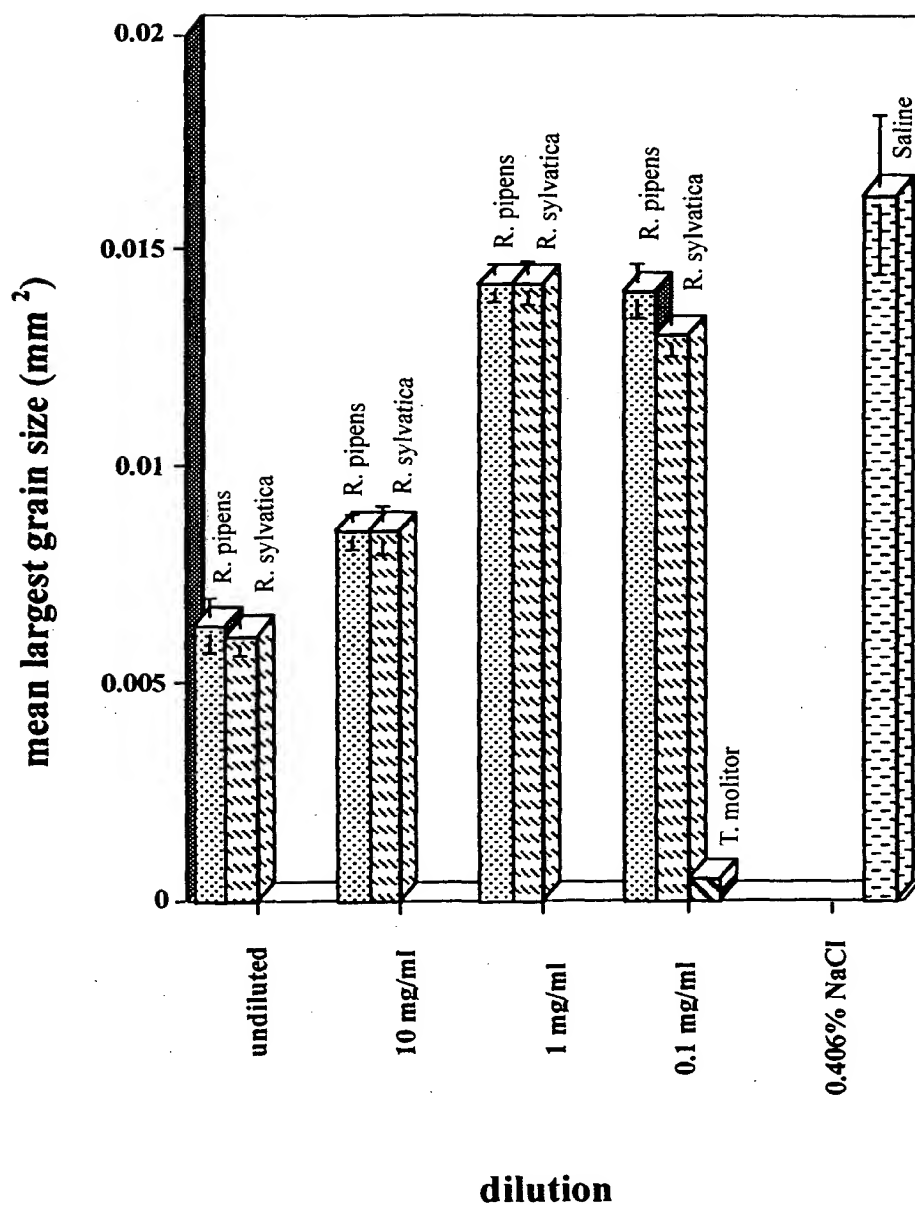


Fig. 8.32

205210 "BHE 92850

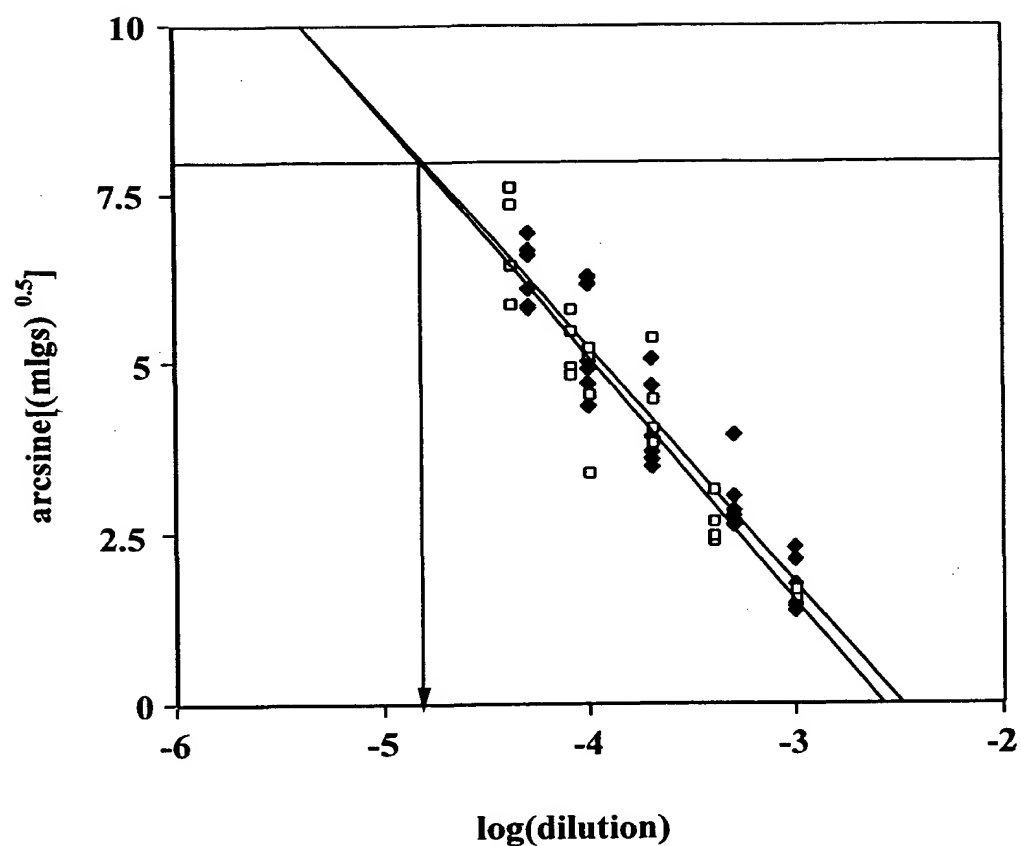


Fig. 8.33

203213 Ste 92860

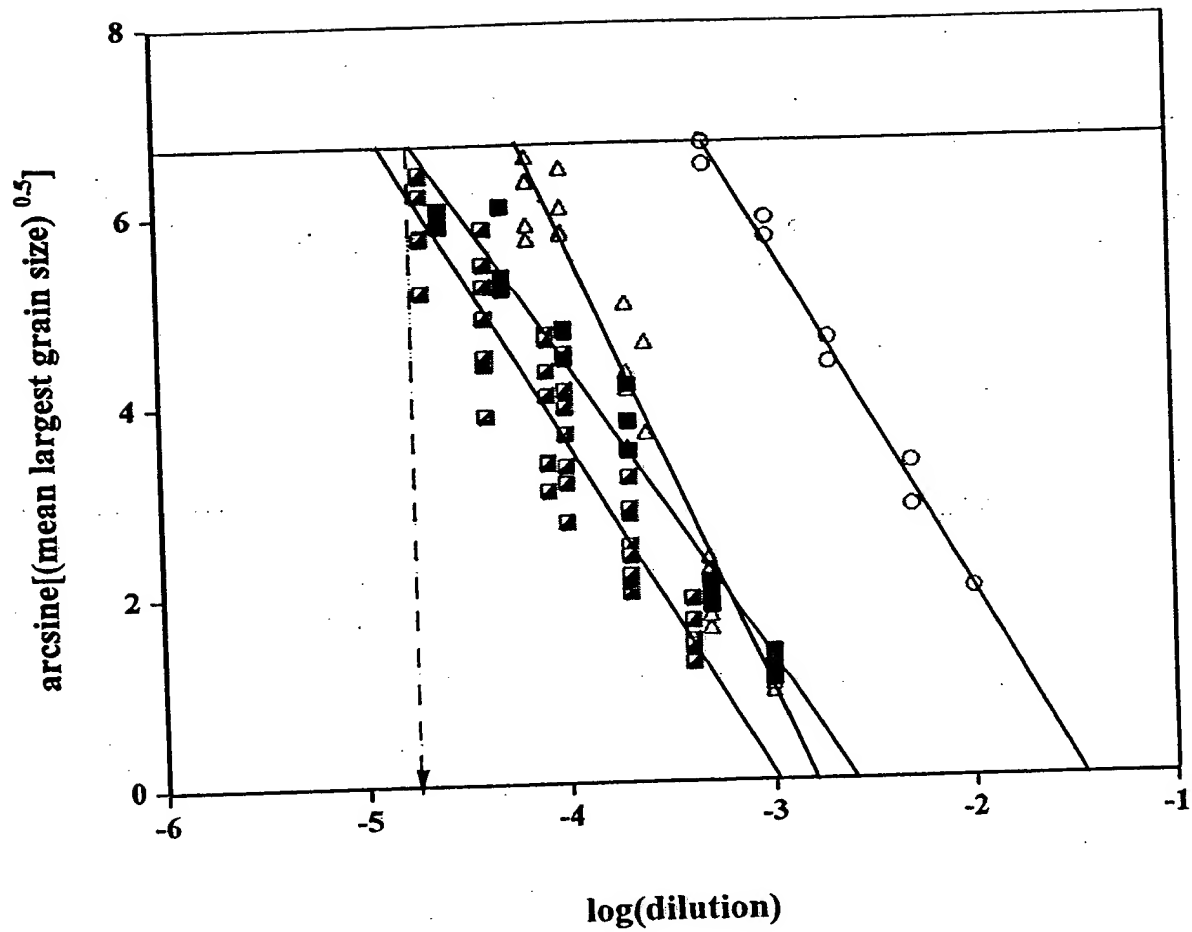


Fig. 8.34

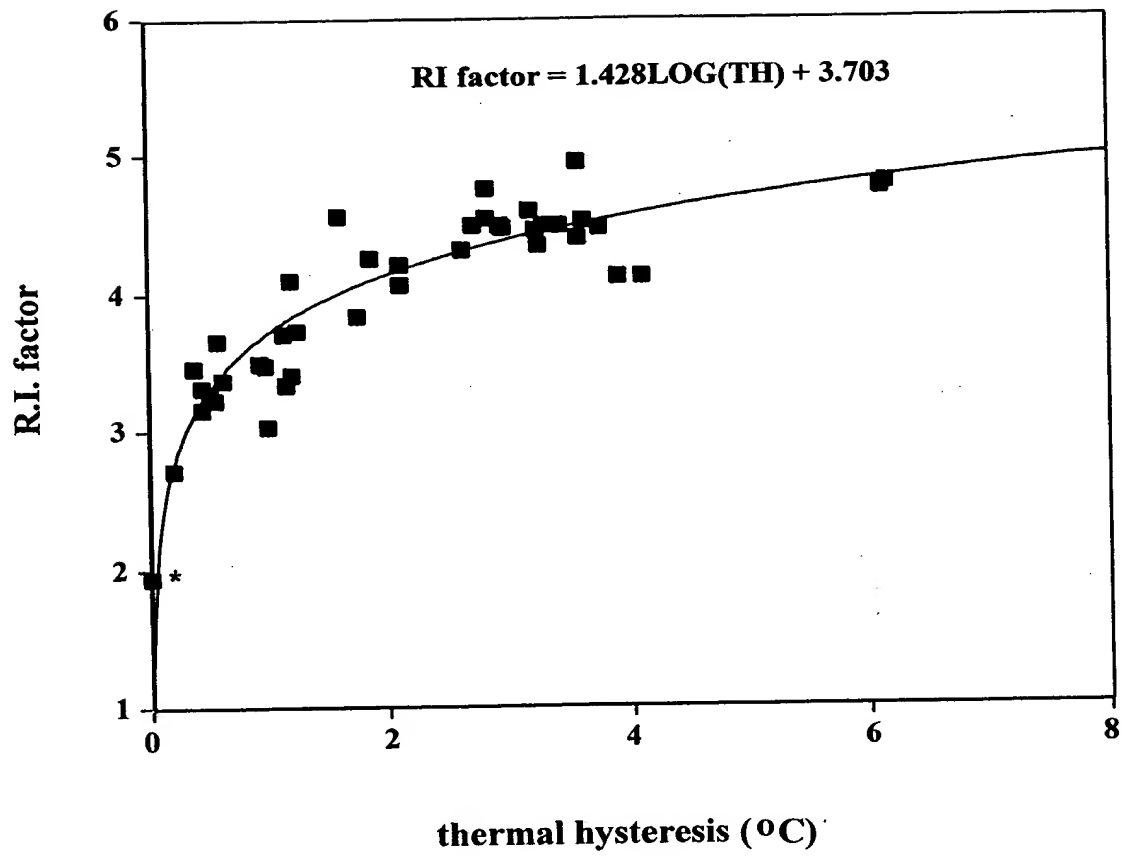


Fig. 8.35

20250101 09:23:00

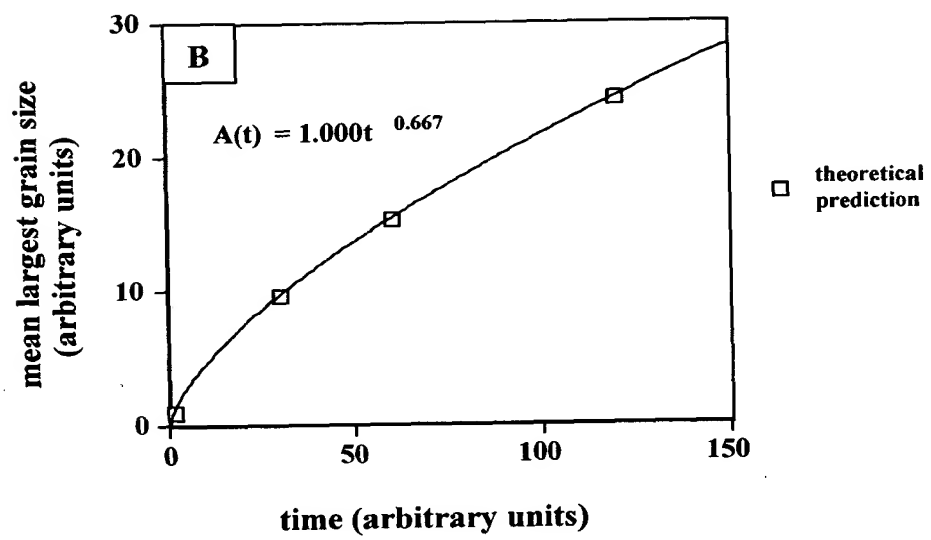
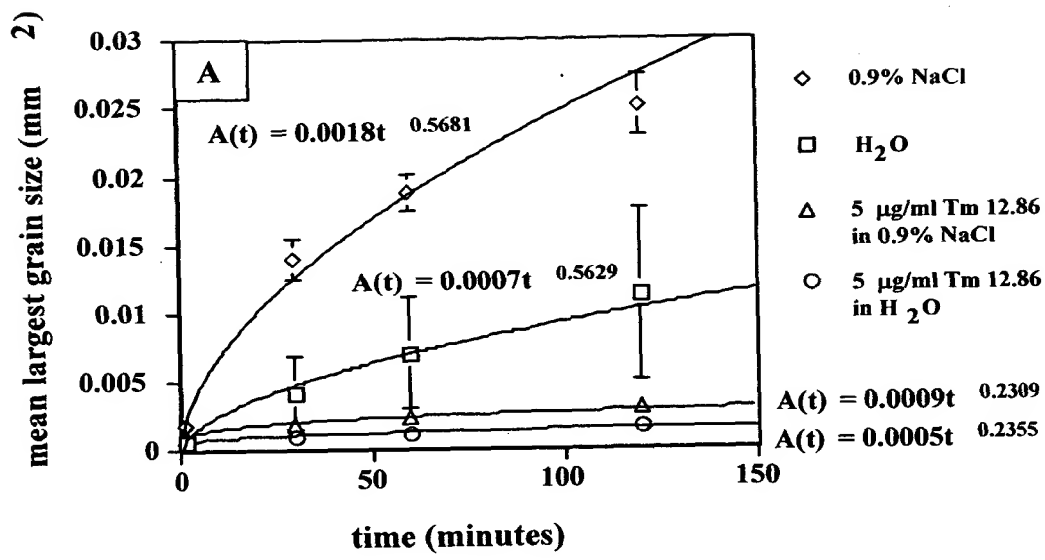


Fig. 8.36

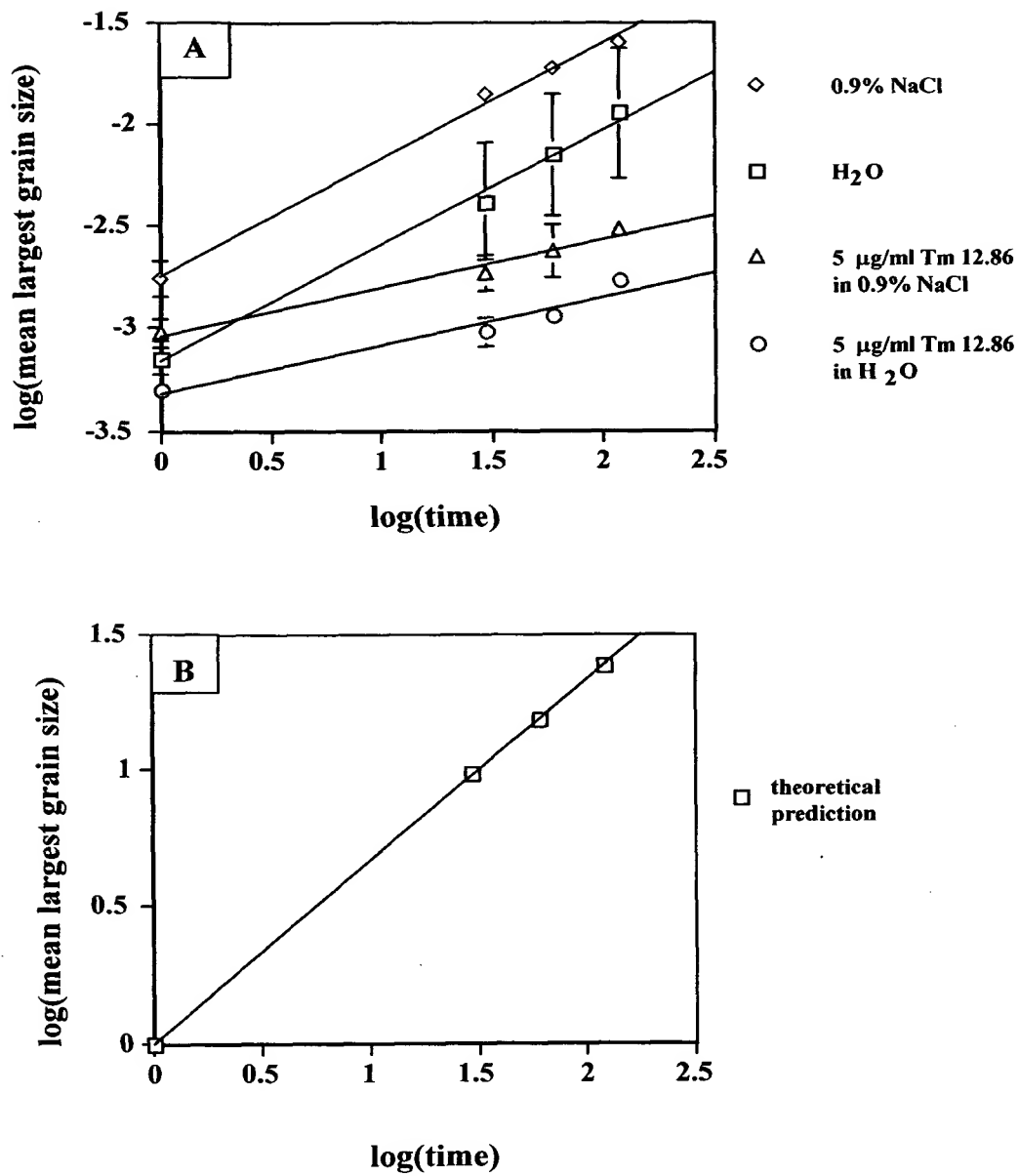
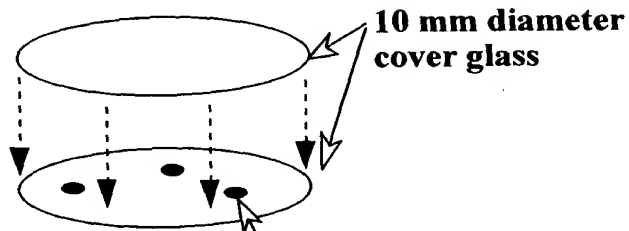


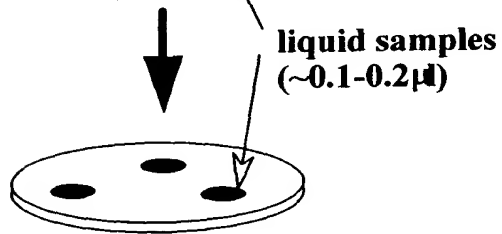
Fig. 8.37

"Sandwich" method of R.I. assessment

1.



2.



**3. FREEZE ON ~ -80 C
ALUMINUM PLATE (~ 10 MIN.)**

**4. PLACE ON COLD STAGE,
ANNEAL AT -6 C UP TO
12+ HOURS**

Fig. 8.38

09075349, 042309

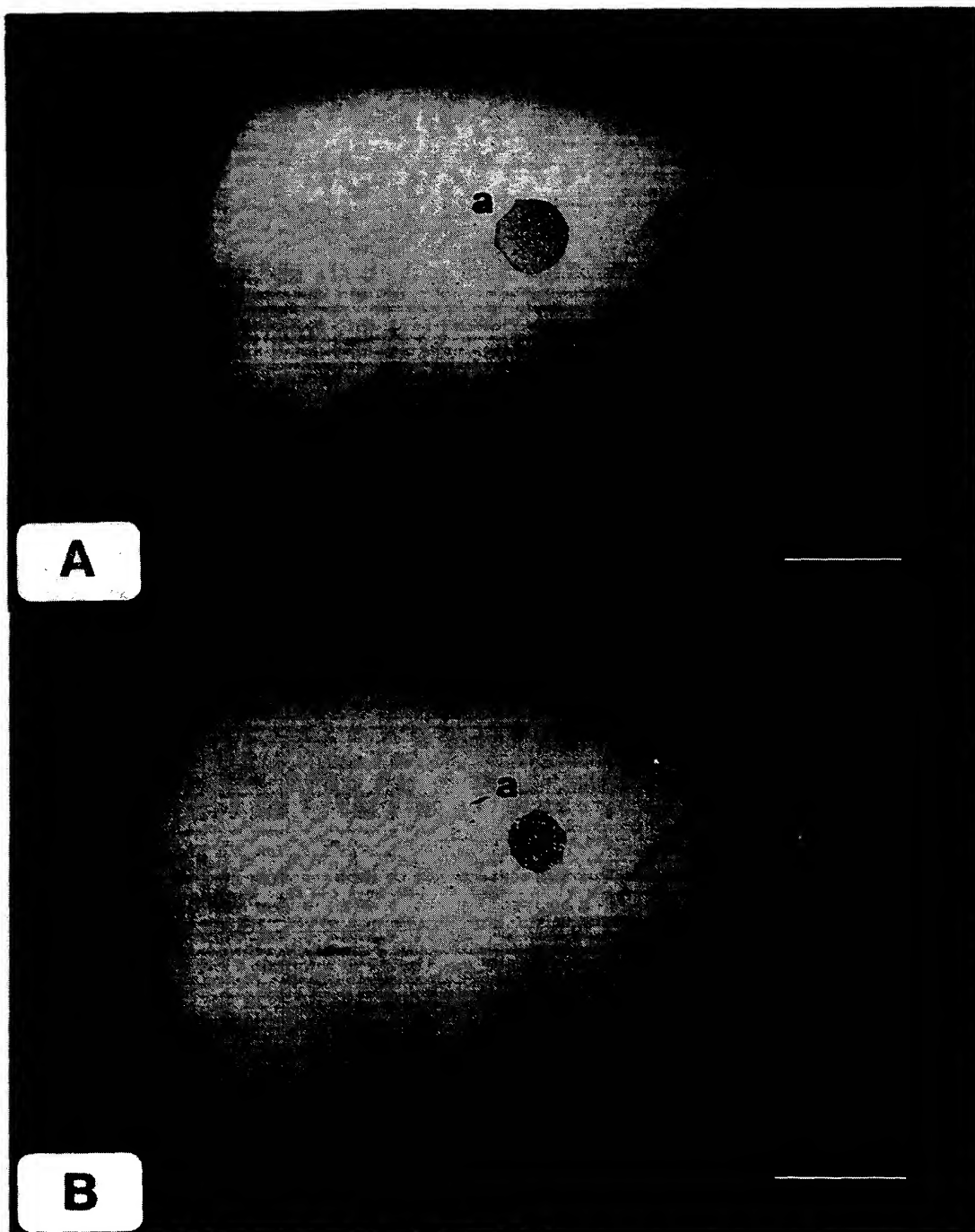


Fig. 8.39

20270 01252560

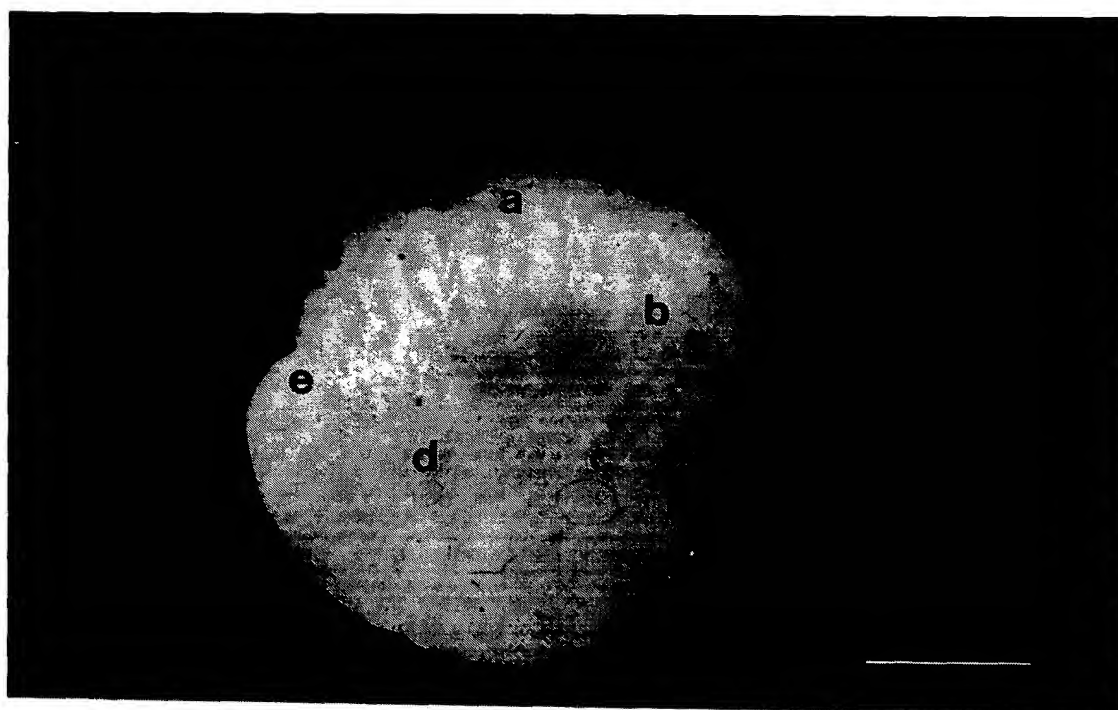


Fig. 8.40

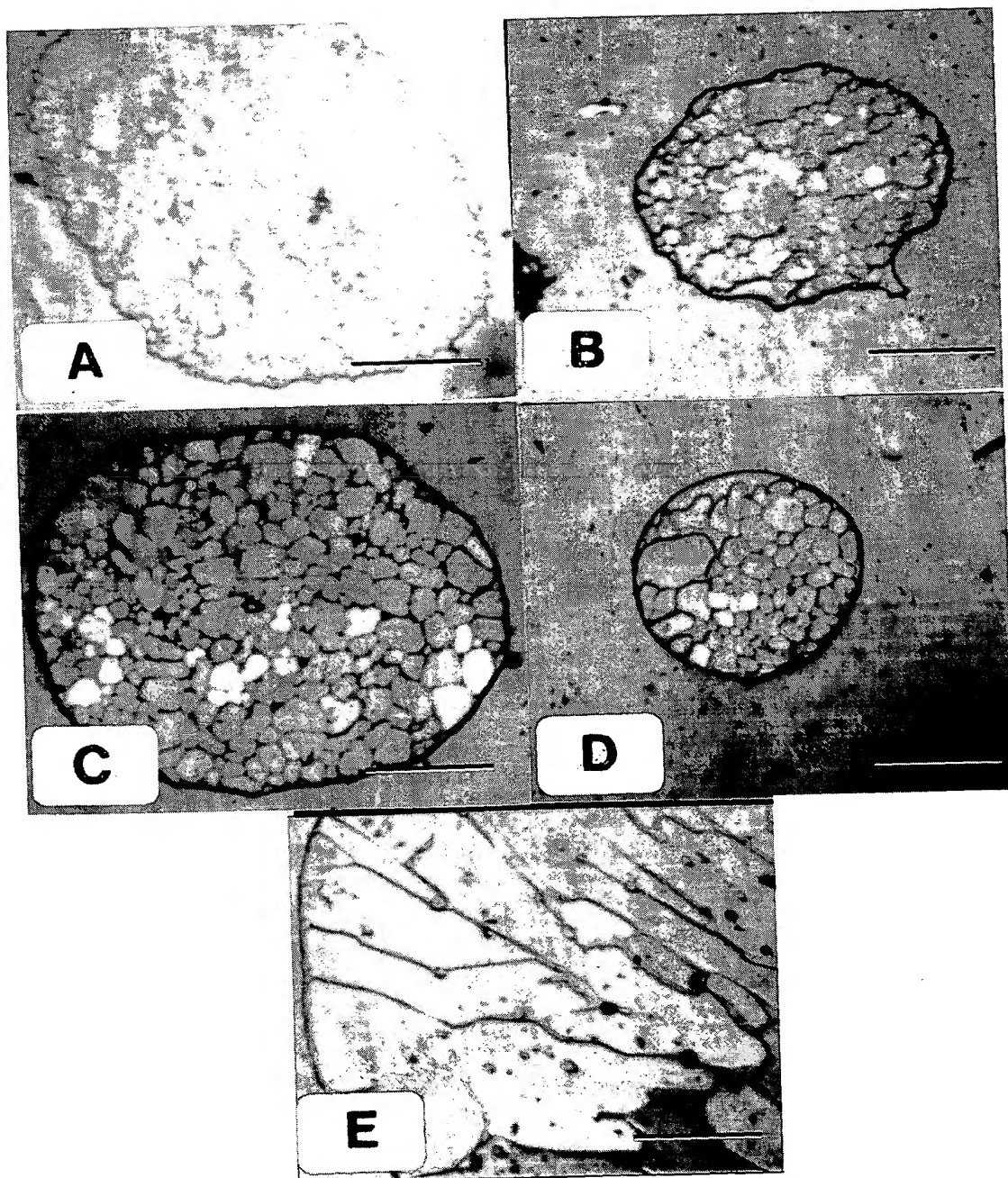


Fig. 8.41

09876543210 0123456789

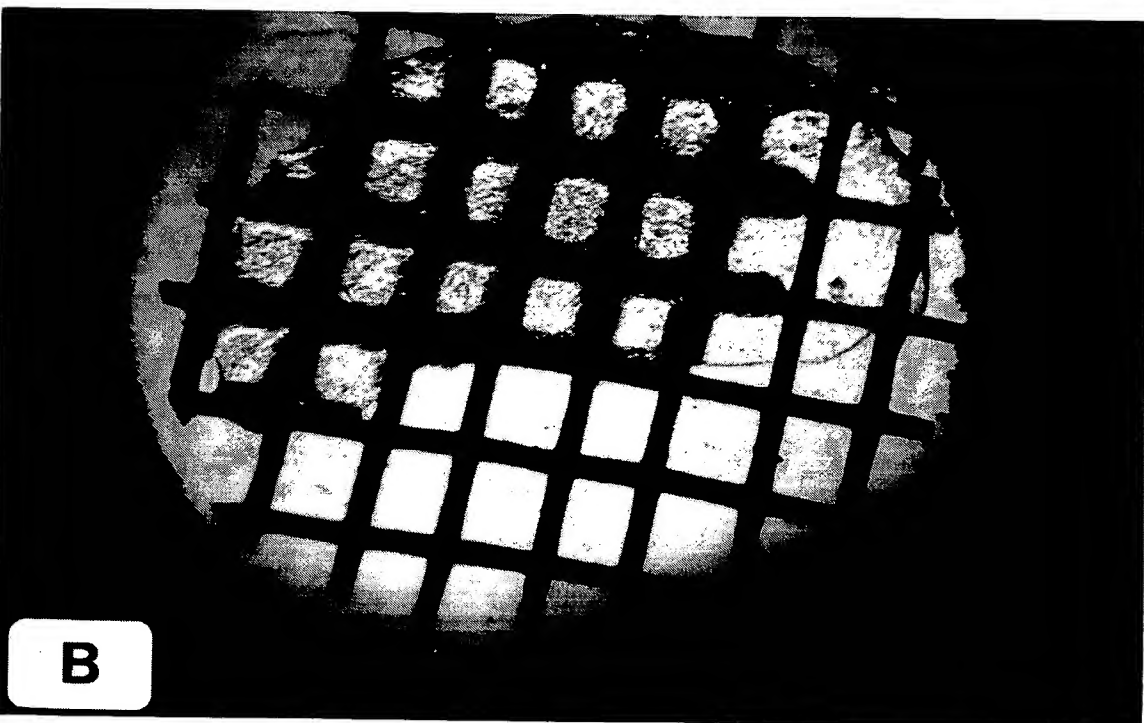
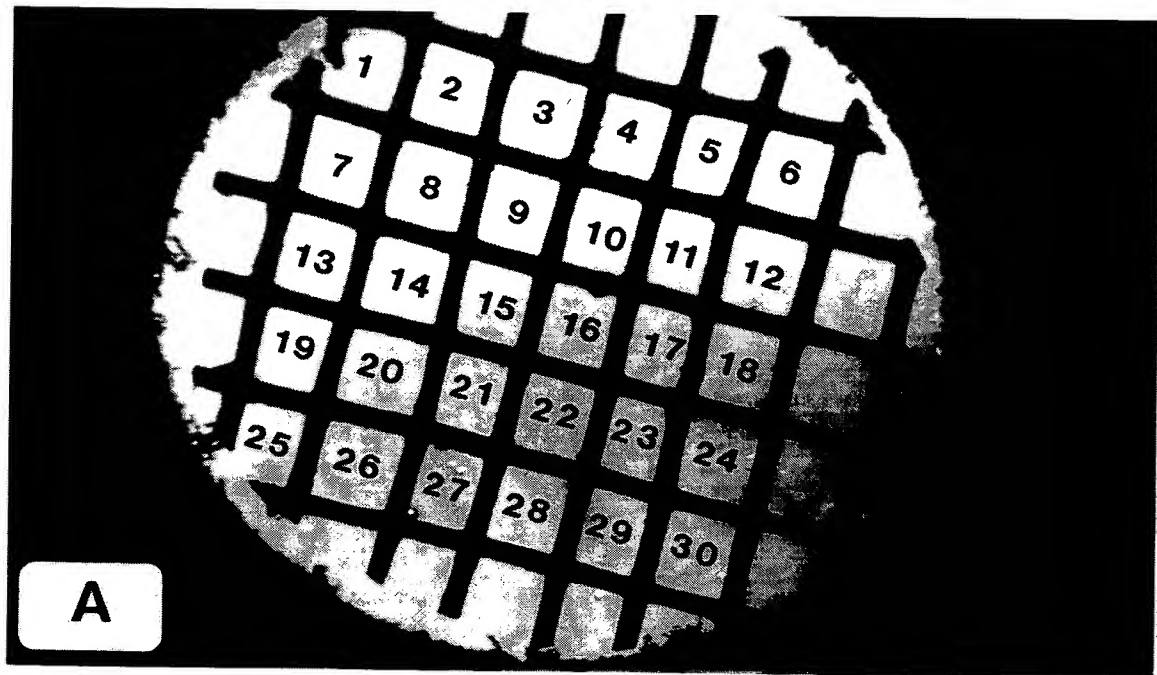


Fig. 8.42

DNA sequence of Tm 13.17 cDNA clone

B E
 a c
 m o
 H R
 I I

1 AGTGGATCCAAAGAATTCCGGCACGAGACTACTAAGATGAAGTTGCTCTGTTGTCTAATCT
 M K L L C C L I S

61 CCCTCATTCTGTTGGTCACAGTTCAGGCCCTGACCGAGGCACAANTTGAGAACTGAACA
 L I L L V T V Q A L T E A Q I E K L N K

121 AGATCAGCAAAAAATGTCAAAATGAAAGTGGAGTGTGCGCAAGGATCATAACCAAGCTC
 I S K K C Q N E S G V S Q E I I T K A R

181 GCAACGGTGACTGGGAGGACGATCCTAAACTGAAACGCCAAGTTTTTTCCTGGCCAGGA
 N G D W E D D P K L K R Q V F C V A R N

241 ACGCCGGTCTGGCCACGGAATCGGGAGAGGTGGTGGTCGACGTGTTGAGGGAGAAGGTGA
 A G L A T E S G E V V V D V L R E K V R

301 GGAAGGTCACTGACAACGACGAAGAAACTGAGAAATCATCAATAAGTCCGCCGTCAAGA
 K V T D N D E E T E K I I N K C A V K R

361 GAGATACTGTTGAAGAGACGGTGTTCATACTTTCAAATGTGTCATGAAAAACAAGCCAA
 D T V E E T V F N T F K C V M K N K P K

421 AGTTCTCACCAGTTGATTGAACACCACGACTAGTAGATGGTTCAAATGGTGTGCTTTAC
 F S P V D *

481 ATATAAAAAATAAAGTGTCTGATGTAAAAAATAAAAAAAAAAAAAAAAAAACTCG
 polyadenylation signal poly (A) tail (26)

537 AGAGTATTCTAGAGCGGCCCGGGCCCATCGTTTCCACCC

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Fig. 8.43

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1 GGCACGAGCAAAAATGAAACTCCTCTTGTGCTTTGCGTTGCGCCGCC
M K L L L C F A F A A

47 ATCGTCATCGGAGCTCAGGCTCTCACCGACGAACAGATACAGAAA
I V I G A Q A L T D E Q I Q K

92 AGGAACAAGATCAGCAAAGAATGCCAGCAGGTGTCCGGAGTGTCC
R N K I S K E C Q Q V S G V S

137 CAAGAAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGATGAT
Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAAAACCTGGA
P K M K K H V L C F S K K T G

226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAGGTGGACAAGATCGTG
K L K H V A S D E E V D K I V

316 CAGAAGTGCGTGGTCAAGAAGGCCACACCGAGAGGAAACGGCTTAT
Q K C V V K K A T P E E T A Y

361 GACACCTTCAAGTGTATTTACGACAGCAAACCTGATTTCTCTCCT
D T F K C I Y D S K P D F S P

406 ATTGATTAAATTGTTTTGTATTTGACTGAATTTTGACAATAAAGGT
I D

451 ACTATCGTTATGTAAAAAAAAAAAAAAAAAAAAA

polyadenylation signal

poly (A) tail

Fig. 8.44